

SUMMARIES					
Query No.	Score	Query		Description	Pred. No.
		Match	Length		
1	26	4.5	239 94	Rattus norvegicus pol	8.14e-09
2	26	4.5	239 45	Rattus norvegicus pol	8.14e-09

## ALIGNMENTS

FT	/evidence=EXPERIMENTAL
FT	/rpt_family="trinucleotide"
FT	/label=GGA_GAA_repeats
FT	28..179
FT	/gene="PIGR-Forml"
FT	/note="1 of 2 PCR product subclones. Unlike F2 (GenBank
FT	Accession No. U17367), GGA and GAA tracts are longer and
FT	shorter; d[AA] and ATAGAA junctions are seen."
FT	/replace=""
FT	repeat_region
FT	64..173
FT	/note="contains 36 GAA triplets; a dinucleotide (d[AA]) at
FT	nts 79-80 interrupts the 5th and 6th GAA repeat unit; a
FT	similar interruption occurs in Wistar genomic clone
FT	Lambda2IGR (GenBank Accession Number U08273)."
FT	/rpt_type=TANDEM
FT	/evidence=EXPERIMENTAL
FT	/rpt_family="trinucleotide"
FT	/rpt_unit=GAA-repeat
FT	174..179
FT	/gene="PIGR-Forml"
FT	/note="separates upstream STMSS from a 283 bp 'unit'
FT	(starting here at nt 180) in the 3'UTRs of Fisher rat Grou
P	
FT	1 cDNAs and Wistar rat genomic clone Lambda2IGR (GenBank
FT	Accession No. U08273); absent from F2."
FT	/evidence=EXPERIMENTAL
FT	/label=ATAGAA-junction
FT	misc_feature
FT	180...239
FT	/gene="PIGR-Forml"
FT	/note="sequence match to GenBank Accession Numbers U08273,
FT	U07886 and U02506; Group 2 pig-R cDNAs lack this unit
FT	(GenBank Accession Numbers L22660, U01145, U00762 and
FT	U00763)."
FT	/evidence=EXPERIMENTAL
FT	complement(221..239)
FT	/gene="PIGR-Forml"
FT	/note="primers were from regions flanking STMSS in Fisher
FT	rat Group 1 pig-R cDNAs (GenBank Accession Numbers U02506,
FT	U07886)."
FT	Sequence 239 BP; 120 A; 14 C; 87 G; 18 T; 0 other;
SQ	
	Query Match 4.5%; Score 26; DB 94; Length 239;
	Best Local Similarity 73.2%; Pred. No. 8.14e-09;
	Matches 41; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
Ddb	33 aggagaggagagagagggagggagggaggaagaagaagaagaagaaga 88
DY	57 AGAGGAGGTGGAGGAGGAGGAGGAGGTGAACACAATGCTACTCAAGGAGACGA 112
RESULT	2
LOCUS	RNU17366 239 bp DNA STS 26-JUN-1997
DEFINITION	Rattus norvegicus polymeric immunoglobulin receptor (PIGR-Forml)
gene, 3'UTR, microsatellite.	
ACCESSION	U17366
NID	G603167
KEYWORDS	STS; microsatellite.
SOURCE	Norway rat.
ORGANISM	Rattus norvegicus
REFERENCE	1 (bases 1 to 239)
AUTHORS	Koch,K.S., Fletcher,R.G., Grond,M.P. and Leffert,H.L.
TITLE	A 43-base-pair complementary DNA sequence homology and triplet repeat motif among putative polymeric immunoglobulin receptor messenger RNAs in regenerating rat liver Hepatology 18 (1), 226-228 (1993)
JOURNAL	93315123
MEDLINE	2 (bases 1 to 239)
REFERENCE	Koch,K.S., Gleiberman,A.S., Aoki,T., Leffert,H.L., Feren,A., Jones,A.L. and Fodor,E.J.
AUTHORS	Discordant expression and variable numbers of neighboring GGA- and

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28..179
/gene="PIGR-Forml"
/note="1 of 2 PCR product subclones. Unlike F2 (GenBank Accession No. U17367), GGA and GAA tracts are longer and shorter; d[AA] and ATAGAA junctions are seen."
/replacement=""
64..173
/note="contains 36 GAA triplets; a dinucleotide (d[AA]) at nt 79-80 interrupts the 5th and 6th GAA repeat unit; a similar interruption occurs in Wistar genomic clone Lambda2igr (GenBank Accession Number U08273)."
/rpt_type=tandem
/evidence=experimental
/rpt_family="trinucleotide"
/rpt_unit=GAA-repeat
174..179
/gene="PIGR-Forml"
/note="separates upstream STMSS from a 283 bp 'unit' (starting here at nt 180) in the 3'UTRs of Fisher rat Group 1 cDNAs and Wistar rat genomic clone Lambda2igr (GenBank Accession No. U08273); absent from F2."
/evidence=experimental
/label=ATAGAA-junction
180..239
/gene="PIGR-Forml"
/note="sequence match to GenBank Accession Numbers U08273, U07886 and U02506; Group 2 pig-R cDNAs lack this unit (GenBank Accession Numbers L22660, U01145, U00762 and U00763)."
/evidence=experimental
complement(221..239)
/gene="PIGR-Forml"
/note="primers were from regions flanking STMSS in Fisher rat Group 1 pig-R cDNAs (GenBank Accession Numbers U02506, U07886)."
120 a      14 c      87 g      18 t

BASE COUNT
ORIGIN

Query Match          4.5%; Score 26; DB 45; Length 239;
Best Local Similarity 73.2%; Pred. No. 8,14e-09;
Matches 41; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Ddb    33 agaggagggaggagggaggaggaggaggagaagaagaagaagaagaagaaga 88
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY     57 AGAAGGAGGTGGAGGAGGAGGAGGAGGTGAACACAACACTGTCAAGGAGACGA 112

RESULT 3
LOCUS              RNUL17366            239 bp            DNA                STS             18-MAY-1995
DEFINITION         Rattus norvegicus polymeric immunoglobulin receptor (PIGR-Forml)
ACCESSION           U17366
NID                 5603167
KEYWORDS            STS; microsatellite.
SOURCE              rat.
ORGANISM            Rattus norvegicus
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Rattus.
1 (bases 1 to 239)
Koch,K.S., Gleiberman,A.S., Aoki,T., Leffert,H.L., Feren,A., Jones,A.L. and Todor,E.J.
Discordant expression and variable numbers of neighboring GGA- and GAA-rich triplet repeats in the 3' untranslated regions of two groups of messenger RNAs encoded by the rat polymeric immunoglobulin receptor gene
Nucleic Acids Res. 23 (7), 1098-1112 (1995)
95258315
2 (bases 1 to 239)
Leffert,H.L.
Direct Submission
Submitted (18-NOV-1994) Hyam L. Leffert, Pharmacology/Center Molecular Genetics, University of California at San Diego. Basic JOURNAL
```

Science Building Room 3025, La Jolla, CA 92093-0636, USA  
 Location/Qualifiers  
 1..239  
 /organism="Rattus norvegicus"  
 /strain="Fisher 344"  
 /note="F1 (1 of 2 genomic subclones obtained by PCR; the 2nd is F2)"  
 /clone="pBluescriptIIKS(-)F1"  
 /sex="male"  
 /cell\_type="hepatocyte"  
 /tissue\_type="liver"  
 /dev\_stage="adult"  
 1..239  
 /gene="PIGR-Form1"  
 1..239  
 /note="PIGR-Form1"  
 /gene="PIGR-Form1"  
 /note="agarose gel purified PCR product subcloned into pBS."  
 label=triplet\_repeat  
 1..19  
 /gene="PIGR-Form1"  
 /note="primers were from regions flanking STMSS in Fisher rat Group 1 pig-R cDNAs (GenBank Accession Numbers U02506, U07886)."  
 1..18  
 /gene="PIGR-Form1"  
 /note="sequence match to GenBank Accession Numbers L22660, U00762, U00763, U01145, U07886 and U02506."  
 /evidence=experimental  
 label=CA-rich\_region  
 1..239  
 /gene="PIGR-Form1"  
 /evidence=experimental  
 19..63  
 /note="GGA tract size of F1 > F2 but is - to GGA tract size in Wistar rat genomic clone Lambda21gr (GenBank Accession No. U08273); all genomic GGA tracts are < GGA tract sizes in all Fisher rat pig-R cDNAs."  
 /rpt\_unit=GGA-repeat  
 /rpt\_type=tandem  
 /evidence=experimental  
 /rpt\_family="trinucleotide"  
 19..179  
 /gene="PIGR-Form1"  
 /standard\_name="microsatellite"  
 /note="contains 2 dissimilar triplet repeats (GGA[n=15], GAA[n=36]) represented discordantly in Fisher Group 1 cDNAs (GenBank Accession Numbers U02506, U07886) and U00762 cDNAs (GenBank Accession Numbers L22660, U01145, U00762 and U00763); this region putatively contains at least one S1 nuclease-sensitive site and potentially may be capable of forming non-B, triplex or tetraplex structure"  
 /rpt\_type=tandem  
 /evidence=experimental  
 /rpt\_family="trinucleotide"  
 /label=GGA\_GAA\_repeats  
 28..179  
 /gene="PIGR-Form1"  
 /note="1 of 2 PCR product subclones. Unlike F2 (GenBank Accession No. U17367), GGA and GAA tracts are longer and shorter; d[AA] and ATAGAA junctions are seen."  
 /replace=""  
 64..173  
 /note="contains 36 GAA triplets; a dinucleotide (d[AA]) at nts 79-80 interrupts the 5th and 6th GAA repeat unit; a similar interruption occurs in Wistar genomic clone Lambda21gr (GenBank Accession Number U08273)."  
 /rpt\_type=tandem  
 /evidence=experimental  
 /rpt\_family="trinucleotide"  
 /rpt\_unit=GAA-repeat  
 174..179  
 /gene="PIGR-Form1"

FEATURES  
 source  
 primer\_bind  
 STS  
 primer\_bind  
 misc\_feature  
 repeat\_region  
 repeat\_region  
 allele  
 repeat\_region  
 misc\_feature

Science Building Room 3025, La Jolla, CA 92093-0636, USA  
 Location/Qualifiers  
 1..239  
 /organism="Rattus norvegicus"  
 /strain="Fisher 344"  
 /note="F1 (1 of 2 genomic subclones obtained by PCR; the 2nd is F2)"  
 /clone="pBluescriptIIKS(-)F1"  
 /sex="male"  
 /cell\_type="hepatocyte"  
 /tissue\_type="liver"  
 /dev\_stage="adult"  
 1..239  
 /gene="PIGR-Form1"  
 1..239  
 /note="PIGR-Form1"  
 /gene="PIGR-Form1"  
 /note="agarose gel purified PCR product subcloned into pBS."  
 label=triplet\_repeat  
 1..19  
 /gene="PIGR-Form1"  
 /note="primers were from regions flanking STMSS in Fisher rat Group 1 pig-R cDNAs (GenBank Accession Numbers U02506, U07886)."  
 1..18  
 /gene="PIGR-Form1"  
 /note="sequence match to GenBank Accession Numbers L22660, U00762, U00763, U01145, U07886 and U02506."  
 /evidence=experimental  
 label=CA-rich\_region  
 1..239  
 /gene="PIGR-Form1"  
 /evidence=experimental  
 19..63  
 /note="GGA tract size of F1 > F2 but is - to GGA tract size in Wistar rat genomic clone Lambda21gr (GenBank Accession No. U08273); all genomic GGA tracts are < GGA tract sizes in all Fisher rat pig-R cDNAs."  
 /rpt\_unit=GGA-repeat  
 /rpt\_type=tandem  
 /evidence=experimental  
 /rpt\_family="trinucleotide"  
 19..179  
 /gene="PIGR-Form1"  
 /standard\_name="microsatellite"  
 /note="contains 2 dissimilar triplet repeats (GGA[n=15], GAA[n=36]) represented discordantly in Fisher Group 1 cDNAs (GenBank Accession Numbers U02506, U07886) and U00762 cDNAs (GenBank Accession Numbers L22660, U01145, U00762 and U00763); this region putatively contains at least one S1 nuclease-sensitive site and potentially may be capable of forming non-B, triplex or tetraplex structure"  
 /rpt\_type=tandem  
 /evidence=experimental  
 /rpt\_family="trinucleotide"  
 /label=GGA\_GAA\_repeats  
 28..179  
 /gene="PIGR-Form1"  
 /note="1 of 2 PCR product subclones. Unlike F2 (GenBank Accession No. U17367), GGA and GAA tracts are longer and shorter; d[AA] and ATAGAA junctions are seen."  
 /replace=""  
 64..173  
 /note="contains 36 GAA triplets; a dinucleotide (d[AA]) at nts 79-80 interrupts the 5th and 6th GAA repeat unit; a similar interruption occurs in Wistar genomic clone Lambda21gr (GenBank Accession Number U08273)."  
 /rpt\_type=tandem  
 /evidence=experimental  
 /rpt\_family="trinucleotide"  
 /rpt\_unit=GAA-repeat  
 174..179  
 /gene="PIGR-Form1"

FEATURES  
 source  
 primer\_bind  
 STS  
 primer\_bind  
 misc\_feature  
 repeat\_region  
 repeat\_region  
 allele  
 repeat\_region  
 misc\_feature

BASE COUNT	90 a	38 c	101 g	54 t	4 others
ORIGIN					
Query Match	4.3%;	Score 25;	DB 13;	Length 287;	
Best Local Similarity	93.1%;	Pred. No. 1.50e-07;			
Matches	27;	Conservative	0;	Mismatches 2;	Indels 0; Gaps 0;
Db	80	gaagaagaggaggaggaggaggaggagg 108			
QY	55	GAAGAAGGAGGTGGAGGAGGAGGAGG 83			
RESULT	5				
ID	HS1301667	standard; RNA; EST; 374 BP.			
AC	AA506215;				
NI	92242455				
DT	04-JUL-1997	(Rel. 52, Created)			
DD	12-JUL-1997	(Rel. 52, Last updated, Version 2)			
DE	nh44e07.s1	NCI_CGAP_Pr5 Homo sapiens cDNA clone 955236.			
OS	Homo sapiens (human)				
OC	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.				
RN	[1]				
RP	1-374				
RA	NCI-CGAP;				
RT	"National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index";				
RL	Unpublished.				
CC	Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov Tissue Procurement: David G. Bostwick, M.D., Rodrigo F. Chuauqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center				
CC	Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html				
CC	Length: 786 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 333.				
CC	Location/Qualifiers				
CC	1..374				
CC	/organism="Homo sapiens"				
CC	/note="Vector: pAMP10; mRNA made from normal prostatic epithelial cells, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp."				
CC	/clone="955236"				
CC	/sex="male"				
CC	/tissue_type="prostate"				
CC	/lab_host="DH10B"				
CC	<1..>374				
CC	81 a 51 c 138 g 104 t				
CC	mRNA				
CC	BASE COUNT				
CC	ORIGIN				
CC	Query Match	4.3%;	Score 25;	DB 38;	Length 374;
CC	Best Local Similarity	90.3%;	Pred. No. 1.50e-07;		
CC	Matches	28;	Conservative	0;	Mismatches 3; Indels 0; Gaps 0;
CC	Db	287	gaagaagaggaggaggaggaggaggagg 317		
CC	QY	55	GAAGAAGGAGGTGGAGGAGGAGGAGG 85		
CC	RESULT	7			
CC	LOCUS	GI8033	400 bp	DNA	STS
CC	DEFINITION	human STS SHGC-8829 clone pg-4562.			
CC	ACCESSION	GI8033			
CC	NID	GI215459			
CC	KEYWORDS	STS sequence; primer; sequence tagged site.			
CC	SOURCE	human Plasmid clones, generated from a lymphoblastoid cell line from a human male. Localized to human chromosome 18 by analysis on the NIGMS Human/Rodent Somatic Cell Hybrid Panel #1, Coriell Institute for Medical Research, Camden, NJ 08103.			
CC	ORGANISM	Homo sapiens			
CC	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homiinae; Homo.				
CC	1 (bases 1 to 400)				
CC	Myers, R.M.				
CC	Unpublished (1996)				
CC	Contact: Richard M. Myers				
CC	Stanford Human Genome Center (SHGC)				
CC	Stanford University School of Medicine				
CC	Department of Genetics, M-344, Stanford, CA 94305, USA				
CC	Tel: 4157259687				

Fax: 4157259689  
Email: myers@hgc.stanford.edu

Primer A: CTGCTCAATTCACCATCAGT  
Primer B: GGGGACAGAGAGAAATCTGG  
STS size: 268  
PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds  
Annealing: 66 degrees C for 23 seconds  
Polymerization: 72 degrees C for 30 seconds  
PCR Cycles: 30

Thermal Cycler: Perkin Elmer 9600

Protocol:  
Template: 25 ng  
Primer: each 1 uM  
dNTPs: each 200 uM  
Taq Polymerase: 0.05 units/uL  
Total Vol: 10 uL

Buffer:  
MgCl2: 2.5 mM  
KCl: 50 mM  
Tris-HCl: 20 mM  
pH: 8.3

Chromosome 18.  
Location/Qualifiers  
source 1..400  
STS /organism="Homo sapiens"  
100..367  
primer\_bind /map="18"  
100..120  
primer\_bind /map="18"  
complement(347...367)

BASE COUNT 110 a 75 c 92 g 120 t 3 others

Query Match 4.3%; Score 25; DB 6; Length 400;  
Best Local Similarity 79.1%; Pred. No. 1.50e-07;  
Matches 34; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 25 agaggtgaggaggagctattagggaatgctcagctca 67  
|||||  
60 AGAGGTGGAGGAGGAGGAGAGAGGTGAGACATGCTGACTCA 102

RESULT 8  
LOCUS G09397 431 bp DNA STS 14-AUG-1995  
DEFINITION human STS CHLC.CCT10.P9317 clone CCT10.  
ACCESSION G09397  
NID 9941246  
KEYWORDS STS sequence; primer; sequence tagged site.  
SOURCE human vector-pJCP1 host-E.coli dut+ung+ (DH10B) Marker Selected genomic DNA prepared from xy individual of French nationality.  
ORGANISM Homo sapiens  
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopharygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 431)  
AUTHORS Murray, J., Sheffield, V., Weber, J.L., Duyk, G. and Buetow, K.H.  
TITLE Cooperative Human Linkage Center  
JOURNAL Unpublished (1995)  
COMMENT Synonyms: CCT10, CHLC.CCT10.T9316  
Contact: Dr. Jeffrey C. Murray  
UofI  
The University of Iowa  
Department of Pediatrics, Iowa City, IA 52242, USA  
Tel: (319) 356-3508  
Fax: (319) 356-3347

Primer A: GAGCCTTTTGCATCTCC  
Primer B: GGGTAACAGAGCAAGACCTC  
STS size: 243  
PCR Profile:  
denature: 30 seconds at 94 degrees C  
annealing: 75 seconds at 55 degrees C

Email: jeff-murray@uiowa.edu

Primer A: GTGGCTGTGATTCACCTAC  
Primer B: TCTGTGTTAGTTTGGCACA  
STS size: 177  
PCR Profile:

denature: 30 seconds at 94 degrees C  
annealing: 75 seconds at 55 degrees C  
extension: 15 seconds at 72 degrees C  
PCR cycles: 27  
extension: 6 minutes at 72 degrees C

Protocol:  
Template: 30ng genomic DNA  
Primer: each 1.5 pmole  
dNTPs: each 200 uM  
Taq Polymerase: 0.3 units  
Total Vol: 10 uL

Buffer:  
MgCl2: 1.5mM  
KCl: 50mM  
Tris: 10mM  
pH: 8.3  
Location/Qualifiers  
source 1..431  
STS /organism="Homo sapiens"  
78..254  
primer\_bind 78..97  
primer\_bind complement(234..254)  
BASE COUNT 142 a 61 c 127 g 95 t 6 others  
ORIGIN

Query Match 4.3%; Score 25; DB 4; Length 431;  
Best Local Similarity 87.9%; Pred. No. 1.50e-07;  
Matches 29; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Db 164 aagagagagagagagagagagagagagagag 196  
|||||  
QY 56 AAGAAGAGGTGGAGGAGGAGGAGAGGTGAAG 88

RESULT 9  
LOCUS G09540 555 bp DNA STS 14-AUG-1995  
DEFINITION human STS CHLC.GCT6H01.P11096 clone GCT6H01.  
ACCESSION G09540  
NID 9941389  
KEYWORDS STS sequence; primer; sequence tagged site.  
SOURCE human vector-pJCP1 host-E.coli dut+ung+ (DH10B) Marker Selected genomic DNA prepared from xy individual of French nationality.  
ORGANISM Homo sapiens  
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopharygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 555)  
AUTHORS Murray, J., Sheffield, V., Weber, J.L., Duyk, G. and Buetow, K.H.  
TITLE Cooperative Human Linkage Center  
JOURNAL Unpublished (1995)  
COMMENT Synonyms: GCT6H01, CHLC.GCT6H01.T11095  
Contact: Dr. Jeffrey C. Murray  
UofI  
The University of Iowa  
Department of Pediatrics, Iowa City, IA 52242, USA  
Tel: (319) 356-3508  
Fax: (319) 356-3347  
Email: jeff-murray@uiowa.edu

Primer A: GAGCCTTTTGCATCTCC  
Primer B: GGGTAACAGAGCAAGACCTC  
STS size: 243  
PCR Profile:  
denature: 30 seconds at 94 degrees C  
annealing: 75 seconds at 55 degrees C

extension: 15 seconds at 72 degrees C  
 PCR cycles: 27  
 extension: 6 minutes at 72 degrees C  
 Template: 30ng genomic DNA  
 Primer: each 1.5 pmole  
 dNTPs: each 200 uM  
 Taq Polymerase: 0.3 units  
 Total Vol: 10 ul

Protocol:

Buffer: MgCl2: 1.5mM  
 KCl: 50mM  
 Tris: 10mM  
 pH: 8.3  
 Location/Qualifiers  
 1..555  
 /organism="Homo sapiens"  
 75..317  
 primer\_bind  
 primer\_bind complement(298..317)  
 COUNT 106 a 128 c 101 g 182 t 38 others

FEATURES

source

STS

primer\_bind

primer\_bind

complement(298..317)

COUNT 106 a 128 c 101 g 182 t 38 others

Query Match

Best Local Similarity 4.3%; Score 25; DB 4; Length 555;

Mismatches 0; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 207 tcttctctctctctctctctctctctctctctctc 241

||||| ||||||| ||||||| ||||||| |||||||

Cp 89 TCTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTC 55

RESULT 10

LOCUS

DEFINITION

TgSTzy20h10.r1 Tgrh Tachyzoite cDNA Toxoplasma gondii cDNA clone

gzy20h10.r1 5'

ACCESSION

N60626

NID

g1206777

EST

TOXOPLASMA GONDII

TOXOPLASMA GONDII

Eukaryotae; Mitochondrial eukaryotes; Alveolata; Apicomplexa;

Coccidia; Eimeriida; Sarcocystidae; Toxoplasma.

1 (bases 1 to 307)

Ajioka, J.A., Aslett, M.A., Dietrich, N., Dubuque, T., Hillier, L.,

Kucaba, T., Marra, M., Sibley, L.D., Wan, K.L. and Waterston, R.H.

WashU-Merck Toxoplasma EST Project

Unpublished (1996)

Contact: Marra M

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: toxo@wustl.edu

Clones can be obtained from Genome Systems Inc. (genome@mo.net);

Library can be obtained from Jim Ajioka (jwa@moie.bio.cam.ac.uk)

Seq primer: T3

High quality sequence stop: 285.

Location/Qualifiers

1..307

/organism="Toxoplasma gondii"

/strain="RH"

/note="Vector: Lambda ZAP; Site\_1: EcoRI; Site\_2: XhoI;

Toxoplasma RH strain tachyzoites were grown in human

foreskin fibroblast cultures in vitro. The library was

constructed by K.L. Wan, Cambridge University. cDNAs were

synthesized from polyA RNAs by oligo d(T) priming and

directionally cloned into the EcoRI to XhoI sites of the

Lambda ZapII vector using the ZAP-cDNA synthesis kit

(Stratagene). WARNING: the library contains a small

(Stratagene).

percentage of cDNAs derived from the human host cells."  
 /clone="tgzy20h10.r1"  
 /clone\_lib="Tgrh Tachyzoite cDNA"  
 /lab\_host="XLI-Blue MRF"  
 <1..>307

BASE COUNT 84 a 59 c 93 g 68 t 3 others  
 ORIGIN

Query Match 4.1%; Score 24; DB 17; Length 307;  
 Best Local Similarity 85.3%; Pred. No. 2.54e-06;  
 Matches 29; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 122 gaagaagagagagagagagagagagagagagag 155  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 55 GAAGAAGAGGTGGAGGAGGAGGAGGAGGTGAAG 88

RESULT 11

ID TG26

AC N60626;

NI g1206777

DT 29-FEB-1996 (Rel. 47, Created)

DT 26-JUN-1997 (Rel. 52, Last updated, Version 3)

DE TgSTzy20h10.r1 Tgrh Tachyzoite cDNA Toxoplasma gondii cDNA clone

DE Tgzy20h10.r1 5'

KW EST

OS Toxoplasma gondii

OC Eukaryotae; Mitochondrial eukaryotes; Alveolata; Apicomplexa;

OC Coccidia; Eimeriida; Sarcocystidae; Toxoplasma.

RN [1]

RP 1-307

RA Ajioka J.A., Aslett M.A., Dietrich N., Dubuque T., Hillier L.,

RA Kucaba T., Marra M., Sibley L.D., Wan K.L., Waterston R.H.;

RT "WashU-Merck Toxoplasma EST Project";

RL Unpublished.

CC Contact: Marra M WashU-Merck EST Project Washington University

CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,

CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:

CC toxo@wustl.edu Clones can be obtained from Genome Systems

CC Inc. (genome@mo.net); library can be obtained from Jim Ajioka

CC (jwa@moie.bio.cam.ac.uk) Seq primer: T3 High quality sequence stop:

CC 285.

Key

Location/Qualifiers

1..307

/organism="Toxoplasma gondii"

/strain="RH"

/note="Vector: Lambda ZAP; Site\_1: EcoRI; Site\_2: XhoI;

Toxoplasma RH strain tachyzoites were grown in human

foreskin fibroblast cultures in vitro. The library was

constructed by K.L. Wan, Cambridge University. cDNAs were

synthesized from polyARNAs by oligo d(T) priming and

directionally cloned into the EcoRI to XhoI sites of the

Lambda ZapII vector using the ZAP-cDNA synthesis kit

(Stratagene). WARNING: the library contains a small

percentage of cDNAs derived from the human host cells."

/clone="tgzy20h10.r1"

/clone\_lib="Tgrh Tachyzoite cDNA"

/lab\_host="XLI-Blue MRF"

<1..>307

Seq Sequence 307 BP; 84 A; 59 C; 93 G; 68 T; 3 other;

Query Match 4.1%; Score 24; DB 92; Length 307;

Best Local Similarity 85.3%; Pred. No. 2.54e-06;

Matches 29; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 122 gaagaagagagagagagagagagagagagagag 155

||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 55 GAAGAAGAGGTGGAGGAGGAGGAGGAGGTGAAG 88

RESULT 12

LOCUS

HS2682D9

387 bp

DNA

STS

28-NOV-1994

```

Denaturation: 94 degrees C for 15 seconds
Annealing: 58 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600

Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Taq Polymerase: 0.05 units/ul
Total Vol: 10 ul

Buffer:
MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3

Chromosome 14.
Location/Qualifiers
1..400
/organism="Homo sapiens"
180..382
/map="14"
primer_bind 180..200
/map="14"
primer_bind complement(361..382)
/map="14"

BASE COUNT 112 a 62 c 121 g 80 t 25 others
ORIGIN

Query Match 4.1%; Score 24; DB 4; Length 400;
Best Local Similarity 92.9%; Pred. No. 2.54e-06;
Matches 26; Conservative 0; Mismatches 2; Indels 0;

Ddb 113 aagaaggaggaggaggaggaggaggagg 140
||||| ||||| ||||| ||||| |||||
QY 56 AAGAAGGAGGTGCAGGAGGAGGAGAAGG 83

RESULT 14
LOCUS human STS CHLC.CCT1.P10053 clone CCT1. 14-AUG
DEFINITION human STS CHLC.CCT1.P10053 clone CCT1.
ACCESSION G09443
NID G941292
KEYWORDS STS sequence; primer; sequence tagged site.
SOURCE human vector-pUCPI host-E.coli dut-tung+ (DH10B) Marker S
genomic DNA prepared from XY individual of French nation
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta;
Catarrhini; Hominoidea; Homo.
1 (bases 1 to 429)
Murray, J., Sheffield, V, Weber, J. L., Duyk, G. and Buetow, K.
Cooperative Human Linkage Center
Unpublished (1995)
Synonyms: CCT1, CHLC.CCT1.P10052
Contact: Dr. Jeffrey C. Murray
UofI
The University of Iowa
Department of Pediatrics, Iowa City, IA 52242, USA
Tel: (319) 356-3508
Fax: (319) 356-3347
Email: jeff-murray@uiowa.edu

Primer A: TGCTTCACATTGAGGAGCC
Primer B: GTTCCCTTATGCTGGATT
STS size: 117
PCR Profile:
denature: 30 seconds at 94 degrees C
annealing: 75 seconds at 55 degrees C

```





\*\*\*\*\*

WPAELH (TM)

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MPSICH nn n.a. - n.a. database search, using Smith-Waterman algorithm  
Run on: Feb-19 10:11:56 1998; MasPar time 156.07 Seconds  
1046.228 Million cell updates/sec  
No output not generated.

Title: >US-08-910-733-12  
Description: (1-579) from US08910733.seq  
Perfect Score: 579  
N.A. Sequence: 1 CAGAAGGACCTCTGTCCTA.....TCCAGGAGGACGAGTAGTAC 579  
Comp: GTCTTCTGGAGCAGCAGAT.....AGGTCTCTGCTCATCATG

Scoring table: TABLE default

Nmatch STD : Dbase 0; Query 0

Searched: 397346 seqs, 141010104 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: EST-C  
1:EST197 2:EST198 3:EST199 4:EST200 5:EST201 6:EST202  
7:EST203 8:EST204 9:EST205 10:EST206 11:EST207 12:EST208  
13:EST209 14:EST210 15:EST211 16:EST212 17:EST213  
18:EST214 19:EST215 20:EST216 21:EST217 22:EST218  
23:EST219 24:EST220 25:EST221 26:EST222 27:EST223  
28:EST224 29:EST225 30:EST226 31:EST227 32:EST228  
33:EST229 34:EST230 35:EST231 36:EST232 37:EST233  
38:EST234 39:EST235 40:EST236 41:EST237 42:EST238  
43:EST239 44:EST240 45:EST241 46:EST242 47:EST243  
48:EST244 49:EST245 50:EST246 51:EST247 52:EST248  
53:EST249 54:EST250 55:EST251 56:EST252 57:EST253  
58:EST254 59:EST255 60:EST256 61:EST257 62:EST258  
63:EST259 64:EST260 65:EST261 66:EST262 67:EST263  
68:EST264 69:EST265 70:EST266 71:EST267 72:EST268  
73:EST269 74:EST270 75:EST271 76:EST272 77:EST273  
78:EST274 79:EST275 80:EST276 81:EST277 82:EST278  
83:EST279 84:EST280 85:EST281 86:EST282 87:EST283  
88:EST284 89:EST285 90:EST286 91:EST287 92:EST288  
93:EST289 94:EST290 95:EST291 96:EST292 97:EST293  
98:EST294

Database: EST-D

99:EST295 100:EST296 101:EST297 102:EST298 103:EST299  
104:EST300 105:EST301 106:EST302 107:EST303 108:EST304  
109:EST305 110:EST306 111:EST307 112:EST308 113:EST309  
114:EST310 115:EST311 116:EST312 117:EST313 118:EST314  
119:EST315

Statistics: Mean 10.606; Variance 2.226; scale 4.764

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

Database:

99:EST295 100:EST296 101:EST297 102:EST298 103:EST299  
104:EST300 105:EST301 106:EST302 107:EST303 108:EST304  
109:EST305 110:EST306 111:EST307 112:EST308 113:EST309  
114:EST310 115:EST311 116:EST312 117:EST313 118:EST314  
119:EST315

Statistics: Mean 10.606; Variance 2.226; scale 4.764

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	244	42.1	349	60	AA381142	EST94184 Activated T-	0.00e+00
2	43	7.4	301	37	AA327613	EST30995 Cornea I Hom	7.15e-33
3	27	4.7	513	67	AA414768	vc72b10.s1 Knowles So	1.09e-09
4	25	4.3	258	111	RICS13404A	Rice cDNA, partial se	3.47e-07
5	25	4.3	447	18	AA110445	ml61d06.r1 Stratagene	3.47e-07
6	24	4.1	232	73	AA344012	EST49871 Gall bladder	5.54e-06
7	24	4.1	534	12	AA241374	mw23b05.r1 Soares mou	5.54e-06
8	24	4.1	542	67	AA413832	vc72b10.s1 Knowles So	5.54e-06
9	24	4.1	588	88	AA054719	zk68d04.s1 Soares pre	5.54e-06
10	23	4.0	203	110	RICS10830A	Rice cDNA, partial se	8.15e-05
11	23	4.0	226	109	RICG11126A	Rice cDNA, partial se	8.15e-05
12	23	4.0	242	111	RICS4040A	Rice cDNA, partial se	8.15e-05
13	23	4.0	270	110	RICS0735A	Rice cDNA, partial se	8.15e-05
14	23	4.0	272	112	AA445033	vg57g05.r1 Beddington	8.15e-05
15	23	4.0	275	111	RICS14303A	Rice cDNA, partial se	8.15e-05
16	23	4.0	286	110	RICS10413A	Rice cDNA, partial se	8.15e-05
17	23	4.0	289	111	RICS4688A	Rice cDNA, partial se	8.15e-05
18	23	4.0	296	109	RICG10912A	Rice cDNA, partial se	8.15e-05
19	23	4.0	303	4	AA214819	mu73h08.r1 Stratagene	8.15e-05
20	23	4.0	308	111	RICS2342A	Rice cDNA, partial se	8.15e-05
21	23	4.0	309	110	RICR0440A	Rice cDNA, partial se	8.15e-05
22	23	4.0	323	109	RICG11195A	Rice cDNA, partial se	8.15e-05
23	23	4.0	330	110	RICG1213A	Rice cDNA, partial se	8.15e-05
24	23	4.0	331	109	RICG1058A	Rice cDNA, partial se	8.15e-05
25	23	4.0	350	46	AA269991	va55e07.r1 Soares mou	8.15e-05
26	23	4.0	354	81	AA411362	zv29g09.r1 Soares ova	8.15e-05
27	23	4.0	367	11	AA238683	mx82h11.r1 Soares mou	8.15e-05
28	23	4.0	385	111	RICS14660A	Rice cDNA, partial se	8.15e-05
29	23	4.0	395	7	AA227161	zr20b10.s1 Stratagene	8.15e-05
30	23	4.0	402	111	RICS4292A	Rice cDNA, partial se	8.15e-05
31	23	4.0	402	111	RICS1848A	Rice cDNA, partial se	8.15e-05
32	23	4.0	406	6	AA221237	mw11b02.r1 Soares mou	8.15e-05
33	23	4.0	410	111	RICS2872A	Rice cDNA, partial se	8.15e-05
34	23	4.0	410	111	RICS1750A	Rice cDNA, partial se	8.15e-05
35	23	4.0	419	32	AA316084	EST187957 HCC cell li	8.15e-05
36	23	4.0	421	47	AA272945	va39g06.r1 Soares mou	8.15e-05
37	23	4.0	428	11	AA236110	zs05e11.r1 Soares NDH	8.15e-05
38	23	4.0	457	117	C19433	Rice cDNA, partial se	8.15e-05
39	23	4.0	459	117	C20070	Rice cDNA, partial se	8.15e-05
40	23	4.0	459	117	C20080	Rice cDNA, partial se	8.15e-05
41	23	4.0	502	46	AA268866	va59g07.r1 Soares mou	8.15e-05
42	23	4.0	502	46	AA268866	va59g07.r1 Soares mou	8.15e-05
43	23	4.0	780	64	AA391050	LD09995.5prime LD Dro	8.15e-05
44	22	3.8	556	101	AA439252	LD13764.5prime LD Dro	1.09e-03
45	22	3.8	583	79	AA401892	zt44d09.s1 Soares ova	1.09e-03

ALIGNMENTS

1  
RESULT AA381142 349 bp mRNA EST 21-APR-1997  
LOCUS EST94184 Activated T-cells I Homo sapiens cDNA 5' end similar to  
DEFINITION Interleukin 1 receptor antagonist (GB:X52015).  
ACCESSION AA381142  
NID g2033462  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;  
Homo.  
REFERENCE 1 (bases 1 to 349)  
AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,  
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,  
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man, Wai, C.,  
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,  
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,  
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,

Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl), 3-174 (1995)

96026280

Other ESTs: EST94183 THC166385

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (<http://www.tigr.org/tdb/hgi.html>)

Seq primer: M13 Reverse.

Location/Qualifiers

1..349

/organism="Homo sapiens"

/note="vector: pBluescript SK-; Site\_1: EcoRI; Site\_2:

XhoI"

/clone\_lib="Activated T-cells I"

/cell\_type="T-lymphocyte"

/dev\_stage="adult"

<1..>349

98 a 78 c 78 g 87 t 8 others

BASE COUNT

ORIGIN

Query Match 42.1%; Score 244; DB 60; Length 349;

Best Local Similarity 94.7%; Pred. No. 0.00e+00;

Matches 266; Conservative 0; Mismatches 12; Indels 3; Gaps 3;

Db 69 gagacgatctgccgaccctctggagaaaatccagcaagatgcgaagcttcagaatctgg 128

QY 106 GAGACGATCTGCCGACCCTCTGGGAGAAAATCCAGCAGATGCAGCCTTCAGAACTCGG 165

Db 129 gatgttaaccagaagaccttntatctgagggaacaccactagttgctggatacttgcga 188

QY 166 GATGTTAACGAGAAGACCTTCTATCTGAGGAACCAACCACTAGTGTCTGGATCTTGCAA 225

Db 189 ggaccaaatgtcaatttagaagaagaatagatgtgtaccattgacctcatgctctg 248

QY 226 GGACCAATGTCAATTTAGAAAGAAAGATAGTGGTACCATTGAGCCCTCATGCTCTG 285

Db 249 ttcttgggnatccatnagggaagaatgtgctctgctgtctgtcgaagcttgggtgatgagac 308

QY 286 TTCTTGGGAATCCATGAGGGAAGATGTGCTCTGTCTGTCAGTCT-GGTGATGAGAC 344

Db 309 cagaatcagctttnnaggnagtttaacattaatgaccttag 349

QY 345 CAGACTCCAGCT-GGAGGCAGTT-AACATCAGTACCTGACCTGAG 383

## RESULT

LOCUS

AA327613

EST30995

Cornea I Homo sapiens

cdna 5' end similar to interleukin 1

receptor antagonist (GB:M55646).

ACCESSION

AA327613

NID

g1979878

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

2 301 bp mRNA EST 20-APR-1997

DEFINITION

EST30995 Cornea I Homo sapiens cdna 5' end similar to interleukin 1

receptor antagonist (GB:M55646).

ACCESSION

AA327613

NID

g1979878

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

2 301 bp mRNA EST 20-APR-1997

## REFERENCE

AUTHORS

1 (bases 1 to 301)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,

White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,

Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,

Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,

Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,

Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,

He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,

Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,

Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,

Fraser, C.M. and Venter, J.C.

Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl), 3-174 (1995)

96026280

Other ESTs: THC168458

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (<http://www.tigr.org/tdb/hgi.html>)

Seq primer: M13 Reverse.

Location/Qualifiers

1..301

/organism="Homo sapiens"

/note="Organ: cornea; Vector: pBluescript SK-; Site\_1:

EcoRI; Site\_2: XhoI"

/clone\_lib="Cornea I"

/dev\_stage="adult"

<1..>301

BASE COUNT

ORIGIN

Query Match 7.4%; Score 43; DB 37; Length 301;

Best Local Similarity 100.0%; Pred. No. 7.15e-33;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 cgtcatgtccaaatcttcttctccaggagagagtagtac 43

QY 537 CGTCATGTCCAAATCTTCTTCTCCAGGAGGAGTAGTAC 579

RESULT

LOCUS

AA414768

DEFINITION

vc72b10.s1 Knowles Solter mouse 2 cell Mus musculus cdna clone

780091 5'.

ACCESSION

AA414768

NID

G2074945

KEYWORDS

EST.

SOURCE

house mouse.

Mus musculus

ORGANISM

Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;

Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;

Murinae; Mus.

1 (bases 1 to 513)

REFERENCE

AUTHORS

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

20-APR-1997

EST30995

Cornea I Homo sapiens

cdna 5' end similar to interleukin 1

receptor antagonist (GB:M55646).

ACCESSION

AA327613

NID

g1979878

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

```

Tsukuba Ibaraki
Japan 305
Phone: 0298-38-7441
Fax : 0298-38-7468.
Location/Qualifiers
1..258
/organism="Oryza sativa"
/strain="Nipponbare"
/dev_stage="Green shoot (8 days old)"
35 a 81 c 97 g 40 t 5 others
BASE COUNT
ORIGIN

Query Match 4.3%; Score 25; DB 111; Length 258;
Best Local Similarity 77.3%; Pred. No. 3.47e-07;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Ddb 2 ttntctgactgtgttcgaggagagagagagagagagag 45
||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 39 TTTAGCTGACTGTGTATGAGAGAGAGGTGGAGGAGGAGAAG 82

RESULT 5
LOCUS AAL10445 447 bp mRNA EST 03-FEB-1997
DEFINITION ml61d05.r1 Stratagene mouse testis (#937308) Mus musculus CDNA
clone 516491 5' similar to TR:G587456 G587456 ALX3. ;.
ACCESSION AAL10445
NID g1662213
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryote; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Mus.
1 (bases 1 to 447)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-RHMI Mouse EST Project
Unpublished (1996)

Contact: Marra M/Mouse EST Project
WashU-RHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:310339
Possible reversed clone: similarity on wrong strand
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 404.
Location/Qualifiers
1..447
/organism="Mus musculus"
/strain="Inbred CD-1"
/Note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dt. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor
sequence: 5' GAATTCGACGACGAG 3' -3' adaptor sequence: 5'
CTCAGATTTTTTTTTTTTTTTT 3'"
/clone="516491"
/clone_lib="Stratagene mouse testis (#937308)"
/sex="males"
/dev_stage="10-12 week old"
/lab_host="SOLR (kanamycin resistant)"
<1..>447
170 a 83 c 154 g 40 t
BASE COUNT
ORIGIN

```



[illegible]

[illegible]

s 0;

96

DNA to

seed

Takuji  
e Genome  
pan

s 0;



\*\*\*\*\*  
[Sequence alignment visualization showing gaps and matches between two sequences]  
\*\*\*\*\*  
(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.  
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Distribution rights by IntelliGenetics, Inc.

MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Thu Feb 19 10:09:19 1998; MasPar time 5.84 Seconds  
428.122 Million cell updates/sec  
[Redacted] ar output not generated.

Title: >US-08-910-733-13  
Description: (1-180) from US08910733.pap  
Perfect Score: 1298  
Sequence: 1 MALADLYEYEGGGGEGEDN.....LTNMPDEGMVMTKTFYQDE 180

Scoring table: PAM 150  
Gap 11

Searched: 111726 seqs, 13889129 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-genes30

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22 23:part23

Statistics: Mean 31.298; Variance 121.057; scale 0.259

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Rank	No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1298	100.0	180	17	R91361		Intracellular IL-1 re	2.79e-127
2	1140	87.8	159	3	R15262		Variant IL-1 cytokine	6.13e-110
3	1140	87.8	177	17	R98251		Interleukin-1 recepto	6.13e-110
4	1140	87.8	177	14	R75784		Human IL-1 receptor a	6.13e-110
5	1140	87.8	177	3	R14400		IRAP.	6.13e-110
6	1137	87.6	177	17	R98253		Interleukin-1 recepto	1.31e-109
7	1137	87.6	177	18	R99262		Human interleukin-1 r	1.31e-109
8	1134	87.4	177	17	R98252		Interleukin-1 recepto	2.78e-109
9	1134	87.4	177	18	R99263		Human interleukin-1 r	2.78e-109
10	1131	87.1	159	13	R73642		iCtIL-lra.	5.94e-109
11	1130	87.1	165	3	P93616		Sequence encoded by b	7.64e-109
12	1131	87.1	177	18	R99261		Human interleukin-1 r	5.94e-109
13	1131	87.1	177	13	R73641		IL-lra.	5.94e-109
14	1130	87.1	177	7	R35485		IL-11-2A fragment.	7.64e-109
15	1130	87.1	177	3	P96159		Sequence of interleuk.	7.64e-109
16	1100	84.7	152	7	R35486		IL-1 inhibitor (IL-1i	1.48e-105
17	1095	84.4	152	5	R27495		Native IL-lra polypep	5.20e-105
18	1086	82.1	177	7	R35489		IL-1 inhibitor (IL-1i	7.77e-102
19	996	76.7	177	3	P91515		Sequence of interleuk	3.48e-94
20	419	32.3	190	7	R35484		IL-11 fragment.	4.77e-32

21	419	32.3	90	3	P93625	Sequence of interleuk	4.77e-32
22	230	17.7	269	7	R36531	Mouse IL-1.	1.19e-12
23	228	17.6	154	4	R22124	Sequence of ovine int	1.88e-12
24	229	17.6	266	1	P80788	Bovine interleukin-1	1.50e-12
25	228	17.6	266	4	R22122	Sequence of ovine int	1.88e-12
26	228	17.6	267	4	R23664	Ovine interleukin-1 b	1.88e-12
27	214	16.5	267	11	R63137	Porcine pro-interleuk	4.53e-11
28	209	16.1	150	8	R47552	Sequence of human int	1.40e-10
29	205	15.8	268	8	R42837	Rat IL-lbeta.	3.44e-10
30	205	15.8	268	1	P96018	Interleukin-1 beta Se	4.31e-10
31	204	15.7	154	4	R23668	Interleukin-1 beta Al	4.31e-10
32	204	15.7	154	4	R23669	Interleukin-1 beta Al	4.31e-10
33	203	15.6	159	2	R10613	Hybrid IL-1 beta/alph	5.39e-10
34	201	15.5	153	1	P90473	Human interleukin-1 b	8.44e-10
35	200	15.4	152	4	R23670	Interleukin-1 beta de	1.06e-09
36	200	15.4	153	8	R42445	Interleukin-1 beta.	1.06e-09
37	200	15.4	153	4	R21697	(1-82)-IL-lbeta and (	1.06e-09
38	200	15.4	153	1	R06269	Radioactive iodine la	1.06e-09
39	200	15.4	153	1	R05386	polypeptide with ppsl	1.06e-09
40	200	15.4	153	1	R04209	Interleukin - 1 beta	1.06e-09
41	200	15.4	154	2	P70525	Interleukin-2 encoded	1.06e-09
42	200	15.4	157	2	P94906	Sequence of amino-ter	1.06e-09
43	200	15.4	193	3	P61520	Sequence of new antit	1.06e-09
44	200	15.4	238	8	R42447	Human interleukin-1 b	1.06e-09
45	200	15.4	295	3	P60680	Prepro- and mature in	1.06e-09

ALIGNMENTS

RESULT 1  
ID R91361 standard; Protein; 180 AA.  
AC R91361;  
DT 22-OCT-1996 (first entry)  
DE Intracellular IL-1 receptor antagonist type II.  
KW Intracellular IL-1 receptor antagonist; iCtIL-lra;  
KW secreted IL-1 receptor antagonist; sIL-lra;  
KW interleukin; IL-la; IL-lb; auto-immune disease.  
OS Homo sapiens.  
PN W09612022-A1.  
PD 25-APR-1996.  
PF 12-OCT-1995; E04023.  
PR 13-OCT-1994; IT-MI2097.  
PA (ISTF ) ARS APPLIED RES SYST HOLDING NV.  
PI Colotta F, Mantovani A, Muzio M;  
DR WPI: 96-222008/22.  
DR N-PSDB: T15099.  
PT IL-1 receptor antagonist active against IL-la and -lb - for  
PT treating, preventing or diagnosing auto-immune diseases  
PS Claim 2; Page 22-23; 36pp; English.  
CC An new IL-1 receptor antagonist includes the sequence given in R91360.  
CC The complete iCtIL-lra1 is given in T15099. The protein is  
CC expressed by DNA similar to that encoding the known receptor  
CC inhibitor iCtIL-lra, but having a 63 bp insert between the first  
CC iCtIL-lra specific exon and the internal acceptor site of the first  
CC exon of sIL-lra.  
SQ Sequence 180 AA;  
Query Match 100.0%; Score 1298; DB 17; Length 180;  
Best Local Similarity 100.0%; Pred. No. 2.79e-127;  
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	1	maladyeeggggggednadsketicrpsgrkssmqafriwdvncqktylrnqlva	60
QY	1	MALADLYEYEGGGGEGEDNADSKETICRPSGRKSSKMQAFRIWDVNCQKTYLRNQLVA	60
Db	61	gylgppnvnleekidvvpiephalfilghgkmcslscvksqdetrlqlteavnitdsenr	120
QY	61	GYLGPPNVNLEEKIDVVPIEPHALFLIGHGKMCCLSCVKSGDETRQLQLTEAVNITDSEN	120
Db	121	kqdrfairsdspttsfesaacpgwflctameadpvslnmpdegvmvmtkfyfqed	180
QY	121	KQDRRFAIRSDSGPTTSFESAACPGWFLCTAMEADPVSILNMPDEGMVMTKTFYQDE	180

RESULT 2  
ID R15262 standard; Protein; 159 AA.  
AC R15262;  
DT 13-FEB-1992 (first entry)  
DE Variant IL-1 cytokine inhibitor.  
KW Intracellular; Interleukin-1; cancer; immunosuppressive.  
OS Homo sapiens.  
PN W09117249-A.  
PD 14-NOV-1991.  
PF 10-APR-1991; U02460.  
PR 01-MAY-1990; US-517276.  
PA (CETU) CETUS CORP.  
PA (UYNC) UNIV NORTH CAROLINA.  
PI Haskill JS, Martin G, Ralph P.  
DR WPI; 91-353770/48.  
DR N-PSDB; Q14843.  
PT New Interleukin-1 antagonists - used to diagnose conditions  
Claim 7; Fig 2; 42pp; English.  
The amino acid sequence is that of an intracellular protein having  
cytokine inhibitory activity. It is a variant interleukin-1 (IL-1)  
cytokine inhibitor. The DNA encoding the inhibitor can be used to  
determine the number of copies of the inhibitor gene present per  
cell in various types of cancers and so measure the degree of over-  
amplification. The inhibitor can be administered to patients at high  
risk of developing sepsis or who have already developed it. It may  
also have immunosuppressive effects against rheumatoid arthritis.  
SQ Sequence 159 AA;

Query Match 87.8%; Score 1140; DB 3; Length 159;  
Best Local Similarity 100.0%; Pred. NO. 6.13e-110;  
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 4 eticrpsgrksskmqafriwvndqktfyllrnnqlvagylogpnvnleekidvvpiephal 63  
QY 25 ETICRPSGRKSSKMQAFRIWDVNDQKTFLYLRNNQLVAGYLOGPNVNLEKIDVVP 84  
Db 64 flqihgkmcscvksqgdetrqlqleavnitdlsenkqdkrfafirsdgpttsfesaac 123  
QY 85 FLQIHGKMCSCVKSQGDETRQLQLEAVNITDLSENRKQDKRFRAFIRSDSGPTTSFES 144  
Db 124 pgwflctameadqpsvltmnpdegvmvtfkfyqede 159  
QY 145 PGWFLCTAMEADQPSVLTNMPDEGVMTKFFQDE 180

T 3  
AC R98251 standard; Protein; 177 AA.  
DE 23-SEP-1996 (first entry)  
DE Interleukin-1 receptor antagonist.  
KW Drug delivery; Escherichia coli; Bacillus subtilis;  
KW Lactobacillus; interleukin-1 receptor antagonist; IL-1ra;  
KW septic shock; therapy.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Peptide 1..25  
FT /label- Sig.peptide  
FT /label- Mat.protein 26..177  
PN W09611277-A1.  
PD 18-APR-1996.  
PF 04-OCT-1995; E03921.  
PR 05-OCT-1994; IT-MI2025.  
PA (DOMP) DOMPE SPA.  
PI Boraschi D, Bossu P, Macchia G, Maurizi G, Porzio S;  
PI Ruggiero P, Tagliabue A;  
DR WPI; 96-209858/21.  
DR N-PSDB; T30157.  
PT Engineered microorganisms expressing therapeutic proteins - useful  
PT as therapeutic delivery systems for the treatment of disease.  
PS Disclosure; Fig 4; 77pp; English.

CC Human interleukin-1 receptor antagonist (IL-1ra) (R98251) is  
CC structurally similar to IL-1 and binds with high affinity to the  
CC IL-1 receptor but does not activate target cells. It has potential  
CC as a therapeutic agent for the treatment of inflammatory and  
CC matrix-destruction diseases e.g. septic shock. cDNA (see also  
CC T30157) coding for IL-1ra or for IL-1ra mutants (R98252-53) can be  
CC inserted into a vector to allow expression in Bacillus subtilis  
CC transformants. In vivo administration of these transformants  
CC results in detectable plasma levels of IL-1ra, demonstrating trans-  
CC mucosal absorption of a recombinant therapeutic protein produced by  
CC a microbial host.  
SQ Sequence 177 AA;

Query Match 87.8%; Score 1140; DB 17; Length 177;  
Best Local Similarity 100.0%; Pred. NO. 6.13e-110;  
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 22 eticrpsgrksskmqafriwvndqktfyllrnnqlvagylogpnvnleekidvvpiephal 81  
QY 25 ETICRPSGRKSSKMQAFRIWDVNDQKTFLYLRNNQLVAGYLOGPNVNLEKIDVVP 84  
Db 82 flqihgkmcscvksqgdetrqlqleavnitdlsenkqdkrfafirsdgpttsfesaac 141  
QY 85 FLQIHGKMCSCVKSQGDETRQLQLEAVNITDLSENRKQDKRFRAFIRSDSGPTTSFES 144  
Db 142 pgwflctameadqpsvltmnpdegvmvtfkfyqede 177  
QY 145 PGWFLCTAMEADQPSVLTNMPDEGVMTKFFQDE 180

RESULT 4  
ID R75784 standard; Protein; 177 AA.  
AC R75784;  
DT 02-FEB-1996 (first entry)  
DE Human IL-1 receptor antagonist.  
KW tumour necrosis factor alpha; moloney murine leukaemia virus;  
KW rheumatoid arthritis; systemic lupus erythematosus; osteoporosis;  
KW osteogenesis imperfecta; Sjorgen's syndrome; systemic sclerosis;  
KW polymyositis-dermatomyositis; vasculitis syndrome; psoriatic arthritis;  
KW ankylosing spondylitis; Paget's disease; inflammatory bowel disease;  
KW synovocyte; keratinocyte; chondrocyte; polymorphonuclear leukocyte.  
OS Homo sapiens.  
PN W09516353-A1.  
PD 22-JUN-1995.  
PF 12-DEC-1994; U14337.  
PR 14-DEC-1993; US-167642.  
PA (UYPI) UNIV PITTSBURGH.  
PI Evans CH, Robbins PD;  
DR WPI; 95-231292/30.  
DR N-PSDB; 090813.  
PT Systemic gene therapy of connective tissue diseases, e.g. rheumatoid  
PT arthritis - using viral vectors to deliver nucleotide sequences  
PT encoding therapeutic peptides/proteins esp. IL-1 receptor antagonist  
PT protein  
PS Example 6; Page 44; 68pp; English.  
CC This sequence represents interleukin-1 receptor antagonist protein  
CC (IRAP). This protein is a product of activated macrophages. The protein  
CC is also produced in synovocytes, keratinocytes, chondrocytes and  
CC polymorphonuclear leukocytes. IRAP is a weak inhibitor of the biological  
CC activities of IL-1. IRAP production is increased by a variety of  
CC cytokines and other stimuli including IL-1, IL-3, IL-4, IL-10 and tumour  
CC necrosis factor alpha (TNF-alpha). The cDNA encoding this sequence can  
CC be introduced into a moloney murine leukaemia virus (MOMLV) vector. This  
CC vector can then be used in methods of treating a variety of autoimmune  
CC and non-autoimmune diseases involving pathogenesis of connective tissue  
CC which promotes inflammation, cytokine mediation and tissue destruction.  
CC These conditions include rheumatoid arthritis, systemic lupus  
CC erythematosus, osteogenesis imperfecta, osteoporosis, Sjorgen's syndrome,  
CC polymyositis-dermatomyositis, systemic sclerosis, vasculitis syndromes,  
CC juvenile rheumatoid arthritis, ankylosing spondylitis, psoriatic  
CC arthritis, Paget's disease and inflammatory bowel disease. The advantage  
CC of using a vector containing IRAP is that it can be used to provide

CC multiple delivery sites, and prolonged activity of the protein within the  
CC patient, which are problems encountered with current methods.  
SQ Sequence 177 AA;

Query Match 87.8%; Score 1140; DB 14; Length 177;  
Best Local Similarity 100.0%; Pred. No. 6.13e-110; Mismatches 0; Indels 0; Gaps 0;  
Matches 156; Conservative 0;

Db 22 eticrpsgrksskmqafriwvngkftfyrnnqlvlgpnvnleekidvvpiephal 81

QY 25 ETICRPSGRKSSKMQAFRIWDVNGKFTFYRNQLVAGYLGPNVNLEEKIDVVP IEPHAL 84

Db 82 flighgkmcclscvsgdetrqlqleavnidlsenrkqdkrfafirsdspttsfesaac 141

QY 85 FLIGHGKMCCLSCVSGDETRQLQLEAVNITDLSNRKQDKRFAFIRSDSGPTTSFESAAC 144

Db 142 pgwflectameadqpsvltmnpdegvmvtkfyfqed 177

QY 145 PGWFLECTAMEADQPSVLTNMPDEGVMTKFFQDE 180

IT 5

R14400 standard; Protein; 177 AA.

AC R14400;

DI 17-FEB-1992 (first entry)

DE IRAP.

OS Scavo peptide; MIRAP; interleukin; receptor; inhibitor.

OS Homo sapiens.

PH Key Location/Qualifiers

FT Peptide 1..15

FT /label= sig\_peptide

FT Protein 26..177

FT /label= mat\_protein

FT Modified\_site 109

FT /label= N-glycosylation\_site

PN W09117184-A.

PD 14-NOV-1991.

PF 03-APR-1991; U02127.

PR 27-APR-1990; US-515468.

PA (URJO ) UPJOHN CO.

PI Carter DB;

DR WPI; 91-353724/48.

DR N-PSDB; Q14693.

PT New DNA molecules are modified Interleukin-1 inhibitors -

PT comprising an IL-1 receptor antagonist protein and a Scavo

PT protein, useful for treating arthritis

PS Disclosure: Page 25, 29pp; English.

CC In order to construct improved Interleukin-1 Receptor Agonist

CC Protein (IRAP), manipulations are performed on the IRAP gene to

CC insert oligonucleotides (Q14690-92) that encode a Scavo peptide

CC into the appropriate region of the IRAP gene.

CC See also Q14690-4.

CC Sequence 177 AA;

Query Match 87.8%; Score 1140; DB 3; Length 177;

Best Local Similarity 100.0%; Pred. No. 6.13e-110;

Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 22 eticrpsgrksskmqafriwvngkftfyrnnqlvlgpnvnleekidvvpiephal 81

QY 25 ETICRPSGRKSSKMQAFRIWDVNGKFTFYRNQLVAGYLGPNVNLEEKIDVVP IEPHAL 84

Db 82 flighgkmcclscvsgdetrqlqleavnidlsenrkqdkrfafirsdspttsfesaac 141

QY 85 FLIGHGKMCCLSCVSGDETRQLQLEAVNITDLSNRKQDKRFAFIRSDSGPTTSFESAAC 144

Db 142 pgwflectameadqpsvltmnpdegvmvtkfyfqed 177

QY 145 PGWFLECTAMEADQPSVLTNMPDEGVMTKFFQDE 180

RESULT 6

ID R98253 standard; Protein; 177 AA.

R98253;  
23-SEP-1996 (first entry)  
DE Interleukin-1 receptor antagonist T109A mutant.  
KW Drug delivery; Escherichia coli; Bacillus subtilis;  
KW Lactobacillus; Interleukin-1 receptor antagonist; IL-1ra;  
KW septic shock; therapy.  
OS Synthetic.  
FH Key Location/Qualifiers  
FT Peptide 1..25  
FT /label= sig\_peptide  
FT Protein 26..177  
FT /label= Mat\_protein  
FT /note= "T109A mutant refers to position 109  
of the mature protein (134 of the  
full-length sequence)"  
PN W09611277-A1.  
PD 18-APR-1996.  
PF 04-OCT-1995; E03921.  
PR 05-OCT-1994; IT-MI2025.  
PA (DOMP-) DOMPE SPA.  
PI Boraschi D, Bossu P, Macchia G, Maurizi G, Porzio S;  
PI Ruggiero P, Tagliabue A;  
DR WPI: 96-209858/21.  
DR N-PSDB; T30159.  
DR Engineered microorganisms expressing therapeutic proteins - useful  
as therapeutic delivery systems for the treatment of disease.  
PS Example 2; Fig 4; 77pp; English.  
CC The T109A mutant (R98253) of human interleukin-1 receptor antagonist  
(IL-1ra) (see also R98251) has an alanine residue substituting  
for threonine at position 109 of the mature protein. The mutant  
retains the activity of native IL-1ra, binding with high affinity to  
the IL-1 receptor, and has potential as a therapeutic agent for the  
treatment of inflammatory and matrix-destruction diseases e.g. septic  
shock. cDNA (T30159) coding for the mutant can be inserted into a  
vector to allow expression in Bacillus subtilis transformants. In  
vivo administration of these transformants results in detectable  
plasma levels of IL-1ra, demonstrating trans-mucosal absorption of a  
recombinant therapeutic protein produced by a microbial host.  
SQ Sequence 177 AA;

Query Match 87.6%; Score 1137; DB 17; Length 177;  
Best Local Similarity 99.4%; Pred. No. 1.31e-109;  
Matches 155; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 22 eticrpsgrksskmqafriwvngkftfyrnnqlvlgpnvnleekidvvpiephal 81

QY 25 ETICRPSGRKSSKMQAFRIWDVNGKFTFYRNQLVAGYLGPNVNLEEKIDVVP IEPHAL 84

Db 82 flighgkmcclscvsgdetrqlqleavnidlsenrkqdkrfafirsdspttsfesaac 141

QY 85 FLIGHGKMCCLSCVSGDETRQLQLEAVNITDLSNRKQDKRFAFIRSDSGPTTSFESAAC 144

Db 142 pgwflectameadqpsvltmnpdegvmvtkfyfqed 177

QY 145 PGWFLECTAMEADQPSVLTNMPDEGVMTKFFQDE 180

RESULT 7

ID R99262 standard; Protein; 177 AA.

AC R99262;

DT 06-NOV-1996 (first entry)

DE Human interleukin-1 receptor antagonist mutant, M1RA-2.

KW Interleukin-1 receptor; antagonist; IL-1; inflammatory disease;

KW rheumatoid arthritis; allergy; graft rejection; autoimmune disease;

KW recombinant; vector.

OS Synthetic.

FH Key Location/Qualifiers

FT Peptide 1..25

FT /label= sig\_peptide

FT Protein 26..177

FT /label= mat\_protein

FT Misc.difference 134

FT /label= substitution

FT /note= "Thr to Ala substitution i.e. Thr appears at  
 PN this position in the wild-type protein"  
 PD W09609323-Al.  
 PF 28-MAR-1996.  
 PR 20-SEP-1995; E03708.  
 PR 21-SEP-1994; IT-M11916.  
 PA (DOMP-) DOMPE SPA.  
 PI Boraschi D, Bossu P, Frascotti G, Frigerio F, Grandi G;  
 PI Grifantini R, Macchia G, Ruggiero P, Tagliabue A;  
 DR WPI; 96-188402/19.  
 DR N-PSDB; T35255.  
 PT Interleukin-1 receptor antagonist mutants - have enhanced  
 PT inhibitory activity, useful for the treatment of rheumatoid  
 PT arthritis, allergies, graft rejection, etc.  
 PS Claim 1; Page -; 41pp; English.  
 CC R99261-R99263 are mutant versions of a human interleukin-1 (IL-1)  
 CC receptor antagonist protein, MILRA-3, MILRA-2 and MILRA-1 respectively.  
 CC They contain at least one of the following two substitutions: Asn to  
 CC Arg at position 91 of the mature protein or Thr to Ala at position  
 CC 109 of the mature protein. The IL-1 receptor antagonist mutants have  
 CC an improved capacity for interaction with IL-1 receptor type I (largely  
 CC responsible for cell activation in response to IL-1). The mutant  
 CC proteins can be used in the prepn. of drugs capable of antagonising the  
 CC inflammatory, neurological, endocrinological, haematological, metabolic,  
 CC catabolic and immunostimulant effects associated with IL-1, and in  
 CC particular for the treatment of acute or chronic inflammatory  
 CC pathologies e.g. rheumatoid arthritis.  
 SQ Sequence 177 AA;

Query Match 87.68; Score 1137; DB 18; Length 177;  
 Best Local Similarity 99.4%; Pred. No. 1.31e-109;  
 Matches 155; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 22 eticrpsgrksskmqafriwvngkftfyrnnqlvavlgqpnvnleekidvvpiephal 81  
 QY 25 ETICRPSGRKSSKMQAFRIWDVNGKFTFRLNNQLVAVLGQPNVNLKIDVVPPIEPHAL 84  
 Db 82 flighgkmcscvsgdetrqlgleavnitdlsnrkqdkrfafirsdsqgtsfesaac 141  
 QY 85 FLIGHGKMCSCVSGDETRQLGLEAVNITDLSNRKQDKRFRAFIRSDSGPTTSFESAAAC 144  
 Db 142 pgwflctameadqpsvltmnpdegvmvtfkfyqede 177  
 QY 145 PGWFLCTAMEADQPSVLTNMPDEGMVMTKFKYFQEDE 180

RESULT 8  
 ID R98252 standard; Protein; 177 AA.  
 AC R98252;  
 DT 23-SEP-1996 (first entry)  
 DE Interleukin-1 receptor antagonist C91R mutant.  
 KW Drug delivery; Escherichia coli; Bacillus subtilis;  
 KW Lactobacillus; interleukin-1 receptor antagonist; IL-1ra;  
 KW septic shock; therapy.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Peptide 1..25  
 FT /label= Sig\_peptide  
 FT Protein 26..177  
 FT /label= Mat\_protein  
 FT Misc\_difference 116  
 FT /label= substitution  
 FT /note= "Asn to Arg substitution i.e. Asn appears at  
 FT this position in the wild-type protein"  
 PN W09609323-Al.  
 PD 28-MAR-1996.  
 PF 20-SEP-1995; E03708.  
 PR 21-SEP-1994; IT-M11916.  
 PA (DOMP-) DOMPE SPA.  
 PI Boraschi D, Bossu P, Frascotti G, Frigerio F, Grandi G;  
 PI Grifantini R, Macchia G, Ruggiero P, Tagliabue A;  
 DR WPI; 96-188402/19.  
 DR N-PSDB; T35256.  
 PT Interleukin-1 receptor antagonist mutants - have enhanced  
 PT inhibitory activity, useful for the treatment of rheumatoid  
 PT arthritis, allergies, graft rejection, etc.  
 PS Claim 1; Page -; 41pp; English.  
 CC R99261-R99263 are mutant versions of a human interleukin-1 (IL-1)  
 CC receptor antagonist protein, MILRA-3, MILRA-2 and MILRA-1 respectively.  
 CC They contain at least one of the following two substitutions: Asn to  
 CC Arg at position 91 of the mature protein or Thr to Ala at position  
 CC 109 of the mature protein. The IL-1 receptor antagonist mutants have  
 CC an improved capacity for interaction with IL-1 receptor type I (largely  
 CC responsible for cell activation in response to IL-1). The mutant  
 CC proteins can be used in the prepn. of drugs capable of antagonising the  
 CC inflammatory, neurological, endocrinological, haematological, metabolic,  
 CC catabolic and immunostimulant effects associated with IL-1, and in  
 CC particular for the treatment of acute or chronic inflammatory  
 CC pathologies e.g. rheumatoid arthritis.  
 SQ Sequence 177 AA;

Query Match 87.68; Score 1137; DB 18; Length 177;  
 Best Local Similarity 99.4%; Pred. No. 1.31e-109;  
 Matches 155; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 22 eticrpsgrksskmqafriwvngkftfyrnnqlvavlgqpnvnleekidvvpiephal 81  
 QY 25 ETICRPSGRKSSKMQAFRIWDVNGKFTFRLNNQLVAVLGQPNVNLKIDVVPPIEPHAL 84  
 Db 82 flighgkmcscvsgdetrqlgleavnitdlsnrkqdkrfafirsdsqgtsfesaac 141  
 QY 85 FLIGHGKMCSCVSGDETRQLGLEAVNITDLSNRKQDKRFRAFIRSDSGPTTSFESAAAC 144  
 Db 142 pgwflctameadqpsvltmnpdegvmvtfkfyqede 177  
 QY 145 PGWFLCTAMEADQPSVLTNMPDEGMVMTKFKYFQEDE 180

RESULT 8  
 ID R98252 standard; Protein; 177 AA.  
 AC R98252;  
 DT 23-SEP-1996 (first entry)  
 DE Interleukin-1 receptor antagonist C91R mutant.  
 KW Drug delivery; Escherichia coli; Bacillus subtilis;  
 KW Lactobacillus; interleukin-1 receptor antagonist; IL-1ra;  
 KW septic shock; therapy.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Peptide 1..25  
 FT /label= Sig\_peptide  
 FT Protein 26..177  
 FT /label= Mat\_protein  
 FT Misc\_difference 116  
 FT /label= substitution  
 FT /note= "Asn to Arg substitution i.e. Asn appears at  
 FT this position in the wild-type protein"  
 PN W09609323-Al.  
 PD 28-MAR-1996.  
 PF 20-SEP-1995; E03708.  
 PR 21-SEP-1994; IT-M11916.  
 PA (DOMP-) DOMPE SPA.  
 PI Boraschi D, Bossu P, Frascotti G, Frigerio F, Grandi G;  
 PI Grifantini R, Macchia G, Ruggiero P, Tagliabue A;  
 DR WPI; 96-188402/19.  
 DR N-PSDB; T35256.  
 PT Interleukin-1 receptor antagonist mutants - have enhanced  
 PT inhibitory activity, useful for the treatment of rheumatoid  
 PT arthritis, allergies, graft rejection, etc.  
 PS Claim 1; Page -; 41pp; English.  
 CC R99261-R99263 are mutant versions of a human interleukin-1 (IL-1)  
 CC receptor antagonist protein, MILRA-3, MILRA-2 and MILRA-1 respectively.  
 CC They contain at least one of the following two substitutions: Asn to  
 CC Arg at position 91 of the mature protein or Thr to Ala at position  
 CC 109 of the mature protein. The IL-1 receptor antagonist mutants have  
 CC an improved capacity for interaction with IL-1 receptor type I (largely  
 CC responsible for cell activation in response to IL-1). The mutant  
 CC proteins can be used in the prepn. of drugs capable of antagonising the  
 CC inflammatory, neurological, endocrinological, haematological, metabolic,  
 CC catabolic and immunostimulant effects associated with IL-1, and in  
 CC particular for the treatment of acute or chronic inflammatory  
 CC pathologies e.g. rheumatoid arthritis.  
 SQ Sequence 177 AA;

PT as therapeutic delivery systems for the treatment of disease.  
 PS Example 2; Fig 4; 77pp; English.  
 CC The C91R mutant (R98252) of human interleukin-1 receptor antagonist  
 CC (IL-1ra) (see also R98251) has an arginine residue substituting  
 CC for cysteine at position 91 of the mature protein. The mutant  
 CC retains the activity of native IL-1ra, binding with high affinity to  
 CC the IL-1 receptor, and has potential as a therapeutic agent for the  
 CC treatment of inflammatory and matrix-destruction diseases e.g. septic  
 CC shock. cDNA (T30158) coding for the mutant can be inserted into a  
 CC vector to allow expression in Bacillus subtilis transformants. In  
 CC vivo administration of these transformants results in detectable  
 CC plasma levels of IL-1ra, demonstrating trans-mucosal absorption of a  
 CC recombinant therapeutic protein produced by a microbial host.  
 SQ Sequence 177 AA;

Query Match 87.4%; Score 1134; DB 17; Length 177;  
 Best Local Similarity 99.4%; Pred. No. 2.78e-109;  
 Matches 155; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 22 eticrpsgrksskmqafriwvngkftfyrnnqlvavlgqpnvnleekidvvpiephal 81  
 QY 25 ETICRPSGRKSSKMQAFRIWDVNGKFTFRLNNQLVAVLGQPNVNLKIDVVPPIEPHAL 84  
 Db 82 flighgkmcscvsgdetrqlgleavnitdlsnrkqdkrfafirsdsqgtsfesaac 141  
 QY 85 FLIGHGKMCSCVSGDETRQLGLEAVNITDLSNRKQDKRFRAFIRSDSGPTTSFESAAAC 144  
 Db 142 pgwflctameadqpsvltmnpdegvmvtfkfyqede 177  
 QY 145 PGWFLCTAMEADQPSVLTNMPDEGMVMTKFKYFQEDE 180

RESULT 9  
 ID R98263 standard; Protein; 177 AA.  
 AC R98263;  
 DT 06-NOV-1996 (first entry)  
 DE Human interleukin-1 receptor antagonist mutant, MILRA-1.  
 KW Interleukin-1 receptor; antagonist; IL-1; inflammatory disease;  
 KW rheumatoid arthritis; allergy; graft rejection; autoimmune disease;  
 KW recombinant; vector.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Peptide 1..25  
 FT /label= sig\_peptide  
 FT Protein 26..177  
 FT /label= mat\_protein  
 FT Misc\_difference 116  
 FT /label= substitution  
 FT /note= "Asn to Arg substitution i.e. Asn appears at  
 FT this position in the wild-type protein"  
 PN W09609323-Al.  
 PD 28-MAR-1996.  
 PF 20-SEP-1995; E03708.  
 PR 21-SEP-1994; IT-M11916.  
 PA (DOMP-) DOMPE SPA.  
 PI Boraschi D, Bossu P, Frascotti G, Frigerio F, Grandi G;  
 PI Grifantini R, Macchia G, Ruggiero P, Tagliabue A;  
 DR WPI; 96-188402/19.  
 DR N-PSDB; T35256.  
 PT Interleukin-1 receptor antagonist mutants - have enhanced  
 PT inhibitory activity, useful for the treatment of rheumatoid  
 PT arthritis, allergies, graft rejection, etc.  
 PS Claim 1; Page -; 41pp; English.  
 CC R99261-R99263 are mutant versions of a human interleukin-1 (IL-1)  
 CC receptor antagonist protein, MILRA-3, MILRA-2 and MILRA-1 respectively.  
 CC They contain at least one of the following two substitutions: Asn to  
 CC Arg at position 91 of the mature protein or Thr to Ala at position  
 CC 109 of the mature protein. The IL-1 receptor antagonist mutants have  
 CC an improved capacity for interaction with IL-1 receptor type I (largely  
 CC responsible for cell activation in response to IL-1). The mutant  
 CC proteins can be used in the prepn. of drugs capable of antagonising the  
 CC inflammatory, neurological, endocrinological, haematological, metabolic,  
 CC catabolic and immunostimulant effects associated with IL-1, and in

CC particular for the treatment of acute or chronic inflammatory  
 CC Pathologies e.g. rheumatoid arthritis.  
 SQ Sequence 177 AA;

Query Match 87.4%; Score 1134; DB 18; Length 177;  
 Best Local Similarity 99.4%; Pred. No. 2,78e-109;  
 Matches 155; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 22 eticrpsgrksskmafrivdngktylrnnqivagylqgpnvnleekidvvpiephal 81

QY 25 ETICRPSGRKSSKMAFRIVDNGKTYLRNNQIVAGYLGPNVNLLEKIDVVPPIEPHAL 84

Db 82 flghgkmcslscvsgdetrqlqleavnitdlsernkqdkrfafirsdsqpttsfesaac 141

QY 85 FLGHGKMCSLSCVSGDETRQLQLEAVNITDLSERNKQDKRFAFIRSDSGPTTSFESAA 144

Db 142 pgwflctameadqpsvsltnmpdegvmvtkfyfqed 177

QY 145 PGWFLCTAMEADQPVSUTNMPDEGVMTKFFQDE 180

RESULT 10

ID R73642 standard; Protein; 159 AA.

AC R73642;

DT 28-NOV-1995 (first entry)

DE ICIL-1ra.

KW Interleukin-1; receptor antagonist; ovulation prevention; embryo;

OS Implantation; contraceptive.

OS Homo sapiens.

PN W09510288-A.

PD 20-APR-1995.

PF 12-OCT-1994; U11588.

PR 12-OCT-1993; US-136077.

PA (POLA/) POLAN M.

PA (POLA/) POLAN M.

PA (SIMO/) SIMON C.

PI Polan ML; Simon C, Polan M;

DR WPI; 95-169961/22.

DR N-PSDB; Q89793.

PT Method of contraception using interleukin-1 receptor antagonist -

PT prevents ovulation and implantation of embryo, also contraceptive

PT device comprising the antagonist

PS Disclosure; Fig 7; 59pp; English.

CC The sequence is that of the polypeptide ICIL-1ra, an interleukin-1

CC receptor antagonist. This polypeptide can be used in a

CC composition (claimed) to prevent ovulation and implantation of an

CC embryo in a mammalian uterus. The IL-1 receptor antagonist is

CC useful in contraceptive compns. It is also useful after the

CC fertilisation event and provide an alternative to known means of

CC terminating pregnancy post-fertilisation.

CC See also R73641.

SQ Sequence 159 AA;

Query Match 87.1%; Score 1131; DB 13; Length 159;  
 Best Local Similarity 98.7%; Pred. No. 5,94e-109;  
 Matches 154; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 4 eticrpsgrksskmafrivdngktylrnnqivagylqgpnvnleekidvvpiephal 63

QY 25 ETICRPSGRKSSKMAFRIVDNGKTYLRNNQIVAGYLGPNVNLLEKIDVVPPIEPHAL 84

Db 64 flghgkmcslscvsgdetrqlqleavnitdlsernkqdkrfafirsdsqpttsfesaac 123

QY 85 FLGHGKMCSLSCVSGDETRQLQLEAVNITDLSERNKQDKRFAFIRSDSGPTTSFESAA 144

Db 124 pgwflctameadqpsvsltnmpdegvmvtkfyfqed 159

QY 145 PGWFLCTAMEADQPVSUTNMPDEGVMTKFFQDE 180

RESULT 11

ID P93616 standard; Protein; 165 AA.

AC P93616;

DT 14-MAR-1992 (first entry)

DE Sequence encoded by bps 61-600 of interleukin-1 inhibitor

DE (IL-1i) gene.

KW Interleukin-1 inhibitor; inflammation therapy;

OS Immunosuppressive agent; inflamed joint.

OS Homo sapiens.

PN EP-343684-A.

PD 29-NOV-1989.

PD 26-MAY-1989; 109540.

PF 27-MAY-1988; US-199915.

PR 31-AUG-1988; US-238171.

PR 31-AUG-1988; US-238173.

PR 23-SEP-1988; US-248521.

PR 03-NOV-1988; US-266531.

PA (SYNE-) SYNERGEN INC.

PI Hannum CH, Eisenberg SP, Thompson RC, Arend WP, Joslin FG,

PI Sommer A;

DR WPI; 89-349765/48.

DR N-PSDB; N92441.

PT Purified interleukin-1 inhibitor - used as an immuno-suppressing

PT agent or to prevent tissue destruction at sites of inflammation

PS Claim 18; Page 28; 53pp; English.

CC The inventors specifically claim recombinant DNA molecule Grl0-IL1i-

CC 2A; and the interleukin-1 inhibitors IL-1i-X, IL-1i-alpha and IL-1i-

CC beta. The preferred component is cDNA or a genomic polynucleotide

CC sequence. It includes bases 99-557 of Grl0-IL1i-2A (see N92441-

CC N92443). Also claimed is a purified interleukin-1 inhibitor (IL-1i),

CC which is active against 1 or more than 1 of IL-1alpha and IL-1beta.

SQ Sequence 165 AA;

Query Match 87.1%; Score 1130; DB 3; Length 165;

Best Local Similarity 99.4%; Pred. No. 7,64e-109;

Matches 155; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 10 eticrpsgrksskmafrivdngktylrnnqivagylqgpnvnleekidvvpiephal 69

QY 25 ETICRPSGRKSSKMAFRIVDNGKTYLRNNQIVAGYLGPNVNLLEKIDVVPPIEPHAL 84

Db 70 flghgkmcslscvsgdetrqlqleavnitdlsernkqdkrfafirsdsqpttsfesaac 129

QY 85 FLGHGKMCSLSCVSGDETRQLQLEAVNITDLSERNKQDKRFAFIRSDSGPTTSFESAA 144

Db 130 pgwflctameadqpsvsltnmpdegvmvtkfyfqed 165

QY 145 PGWFLCTAMEADQPVSUTNMPDEGVMTKFFQDE 180

RESULT 12

ID R99261 standard; Protein; 177 AA.

AC R99261;

DT 06-NOV-1996 (first entry)

DE Human interleukin-1 receptor antagonist mutant, MILRA-3.

KW Interleukin-1 receptor; antagonist; IL-1; inflammatory disease;

KW rheumatoid arthritis; allergy; graft rejection; autoimmune disease;

KW recombinant; vector.

OS Synthetic.

Key Location/Qualifiers

FT Peptide 1..25

FT /label= sig\_peptide

FT Protein 26..177

FT /label= mat\_protein

FT Misc\_difference 116

FT /label= substitution

FT /note= "Asn to Arg substitution i.e. Asn appears at

FT this position in the wild-type protein"

FT Misc\_difference 134

FT /label= substitution

FT /note= "Thr to Ala substitution i.e. Thr appears at

FT this position in the wild-type protein"

FN W09609323-A1.

PD 28-MAR-1996.

PF 20-SEP-1995; E03708.

PR 21-SEP-1994; IT-MI1916.

(DOMP-) DOMPE SPA.  
 PA Boraschi D, Bossu P, Frascotti G, Frigerio F, Grandi G;  
 PI Grifantini R, Macchia G, Ruggiero P, Tagliabue A;  
 DR WPI: 96-188402/19.  
 DR N-PSDB; T13177.  
 PT Interleukin-1 receptor antagonist mutants - have enhanced  
 PT inhibitory activity, useful for the treatment of rheumatoid  
 PT arthritis, allergies, graft rejection, etc.  
 PS Claim 1; Page 4; 41pp; English.  
 CC R99261-R99263 are mutant versions of a human interleukin-1 (IL-1)  
 CC receptor antagonist protein, IL1RA-3, IL1RA-2 and IL1RA-1 respectively.  
 CC They contain at least one of the following two substitutions: Asn to  
 CC Arg at position 91 of the mature protein or Thr to Ala at position  
 CC 109 of the mature protein. The IL-1 receptor antagonist mutants have  
 CC an improved capacity for interaction with IL-1 receptor type I (largely  
 CC responsible for cell activation in response to IL-1). The mutant  
 CC proteins can be used in the prep. of drugs capable of antagonising the  
 CC inflammatory, neurological, endocrinological, haematological, metabolic,  
 CC catabolic and immunostimulant effects associated with IL-1, and in  
 CC particular for the treatment of acute or chronic inflammatory  
 CC pathologies e.g. rheumatoid arthritis.  
 SQ Sequence 177 AA;  
 Query Match 87.1%; Score 1131; DB 18; Length 177;  
 Best Local Similarity 98.7%; Pred. No. 5.94e-109;  
 Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Db 22 eticrpsgrksskmaqfrlwdvngkftfyrlnnqlvagyvgpnvnleekidvvpiephal 81  
 QY 25 ETICRPSGRKSSKMAQFRlWDVNGKFTfYLRNQLVAGYVGPNVNLEEKIDVVPiEPHAL 84  
 Db 82 flghgkmcslcvsksgdetrqlqleavnitdlsernkqdkrfafirsdsqpttsfesaac 141  
 QY 85 FLGHGKMCslcvsksgdetrqlqleavnitdlsernkqdkrfafirsdsqpttsfESAAC 144  
 Db 142 pgwflctameadqpsvsltnmpdegvmvtfkyfqed 177  
 QY 145 PGWFLCTAMEADQPVSltNMPDEGVMTKfYFQEDE 180  
 RESULT 13  
 ID R73641 standard; Protein; 177 AA.  
 AC R73641;  
 DT 28-NOV-1995 (first entry)  
 DE IL-1ra.  
 KW Interleukin-1; receptor antagonist; ovulation prevention; embryo;  
 KW implantation; contraceptive.  
 KW Homo sapiens.  
 DR W09510298-A.  
 PF 12-OCT-1994; U11588.  
 PR 12-OCT-1993; US-136077.  
 PA (POLA/) POLAN M L.  
 PA (POLA/) POLAN M.  
 PA (SIMO/) SIMON C.  
 PI Polan ML, Simon C, Polan M;  
 DR WPI: 95-169961/22.  
 DR N-PSDB; Q89792.  
 PT Method of contraception using interleukin-1 receptor antagonist -  
 PT prevents ovulation and implantation of embryo, also contraceptive  
 PT device comprising the antagonist  
 PS Disclosure; Fig 6; 59pp; English.  
 CC The sequence is that of the polypeptide IL-1ra, an interleukin-1  
 CC receptor antagonist. This polypeptide can be used in a  
 CC composition (claimed) to prevent ovulation and implantation of an  
 CC embryo in a mammalian uterus. The IL-1 receptor antagonist is  
 CC useful in contraceptive compans. It is also useful after the  
 CC fertilisation event and provide an alternative to known means of  
 CC terminating pregnancy post-fertilisation.  
 CC See also R73642.  
 SQ Sequence 177 AA;  
 Query Match 87.1%; Score 1131; DB 13; Length 177;  
 Best Local Similarity 98.7%; Pred. No. 5.94e-109;  
 Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Db 22 eticrpsgrksskmaqfrlwdvngkftfyrlnnqlvagyvgpnvnleekidvvpiephal 81  
 QY 25 ETICRPSGRKSSKMAQFRlWDVNGKFTfYLRNQLVAGYVGPNVNLEEKIDVVPiEPHAL 84  
 Db 82 flghgkmcslcvsksgdetrqlqleavnitdlsernkqdkrfafirsdsqpttsfesaac 141  
 QY 85 FLGHGKMCslcvsksgdetrqlqleavnitdlsernkqdkrfafirsdsqpttsfESAAC 144  
 Db 142 pgwflctameadqpsvsltnmpdegvmvtfkyfqed 177  
 QY 145 PGWFLCTAMEADQPVSltNMPDEGVMTKfYFQEDE 180  
 RESULT 13  
 ID R73641 standard; Protein; 177 AA.  
 AC R73641;  
 DT 28-NOV-1995 (first entry)  
 DE IL-1ra.  
 KW Interleukin-1; receptor antagonist; ovulation prevention; embryo;  
 KW implantation; contraceptive.  
 KW Homo sapiens.  
 DR W09510298-A.  
 PF 12-OCT-1994; U11588.  
 PR 12-OCT-1993; US-136077.  
 PA (POLA/) POLAN M L.  
 PA (POLA/) POLAN M.  
 PA (SIMO/) SIMON C.  
 PI Polan ML, Simon C, Polan M;  
 DR WPI: 95-169961/22.  
 DR N-PSDB; Q89792.  
 PT Method of contraception using interleukin-1 receptor antagonist -  
 PT prevents ovulation and implantation of embryo, also contraceptive  
 PT device comprising the antagonist  
 PS Disclosure; Fig 6; 59pp; English.  
 CC The sequence is that of the polypeptide IL-1ra, an interleukin-1  
 CC receptor antagonist. This polypeptide can be used in a  
 CC composition (claimed) to prevent ovulation and implantation of an  
 CC embryo in a mammalian uterus. The IL-1 receptor antagonist is  
 CC useful in contraceptive compans. It is also useful after the  
 CC fertilisation event and provide an alternative to known means of  
 CC terminating pregnancy post-fertilisation.  
 CC See also R73642.  
 SQ Sequence 177 AA;  
 Query Match 87.1%; Score 1131; DB 13; Length 177;  
 Best Local Similarity 98.7%; Pred. No. 5.94e-109;  
 Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Db 22 eticrpsgrksskmaqfrlwdvngkftfyrlnnqlvagyvgpnvnleekidvvpiephal 81  
 QY 25 ETICRPSGRKSSKMAQFRlWDVNGKFTfYLRNQLVAGYVGPNVNLEEKIDVVPiEPHAL 84  
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 QY 85 FLGHGKMCslcvsksgdetrqlqleavnitdlsernkqdkrfafirsdsqpttsfESAAC 144

Best Local Similarity 99.4%; Pred. No. 5.94e-109;  
 Matches 155; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Db 22 eticrpsgrksskmaqfrlwdvngkftfyrlnnqlvagyvgpnvnleekidvvpiephal 81  
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 Db 82 flghgkmcslcvsksgdetrqlqleavnitdlsernkqdkrfafirsdsqpttsfesaac 141  
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 Db 142 pgwflctameadqpsvsltnmpdegvmvtfkyfqed 177  
 QY 145 PGWFLCTAMEADQPVSltNMPDEGVMTKfYFQEDE 180  
 RESULT 14  
 ID R35485 standard; Protein; 177 AA.  
 AC R35485;  
 DT 26-AUG-1993 (first entry)  
 DE IL-1i-2A fragment.  
 KW Interleukin-1 inhibitor; immunosuppressive; inflammation; cytokine;  
 KW collagenase.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Peptide 1..25  
 FT /note= "part of N-terminal signal sequence;  
 FT claim 12, page 28"  
 FT Protein 26  
 FT /label= IL-1i  
 FT /modified\_site 109  
 FT /note= "N residue that is part of a  
 FT consensus N-glycosylation site"  
 FT Misc\_difference 26  
 FT /note= "P residue; but no P has been  
 FT detected at this position (the N-terminus)  
 FT of form X of IL-1i; this residue may be  
 FT modified in the mature protein"  
 PN EP-541920-A.  
 PD 19-MAY-1993.  
 PF 26-MAY-1989; 109540.  
 PR 27-MAY-1988; US-199915.  
 PR 31-AUG-1988; US-238713.  
 PR 23-SEP-1988; US-248521.  
 PR 03-NOV-1988; US-266531.  
 PA (SYND ) SYNERGEN INC.  
 PI Arend WP, Eisenberg SP, Hannum CH, Joslin FG, Sommer A;  
 PI Thompson RC;  
 DR WPI: 93-160536/20.  
 DR N-PSDB; Q40753.  
 PT New interleukin-1 inhibiting peptide and DNA - useful as  
 PT immunosuppressant for treating auto-immune and other immune  
 PT disorders  
 PS Disclosure; Fig 14; 55pp; English.  
 CC A plaque, GT10-IL-1i-2A, was isolated from a GT10 library, using  
 CC the probes given in Q40757-61.  
 CC IL-1i is useful as an immunosuppressive agent. When applied  
 CC locally it can be used to prevent tissue destruction in an inflamed  
 CC joint and other inflammation sites. This protective effect may be  
 CC improved if IL-1i is given with collagenase inhibitors.  
 SQ Sequence 177 AA;  
 Query Match 87.1%; Score 1130; DB 7; Length 177;  
 Best Local Similarity 99.4%; Pred. No. 7.64e-109;  
 Matches 155; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Db 22 eticrpsgrksskmaqfrlwdvngkftfyrlnnqlvagyvgpnvnleekidvvpiephal 81  
 QY 25 ETICRPSGRKSSKMAQFRlWDVNGKFTfYLRNQLVAGYVGPNVNLEEKIDVVPiEPHAL 84  
 Db 82 flghgkmcslcvsksgdetrqlqleavnitdlsernkqdkrfafirsdsqpttsfesaac 141  
 QY 85 FLGHGKMCslcvsksgdetrqlqleavnitdlsernkqdkrfafirsdsqpttsfESAAC 144

Db 142 pgwflctameadqpsltnmpdegvmvtkfyfgede 177  
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QY 145 PGWFLCTAMEADQPSVLTNMPDEGMVMTKFFQDE 180

RESULT 15

ID P96159 standard; Protein; 177 AA.  
AC P96159;  
DT 14-MAR-1992 (first entry)  
DE Sequence of interleukin-1 inhibitor (IL-1i) encoded by the  
DE protein coding region of lambda GT10-IL1i-2A.  
KW Interleukin-1 inhibitor; inflammation therapy;  
KW immunosuppressive agent; inflamed joint.  
OS Homo sapiens.  
PN EP-343684-A.  
PD 29-NOV-1989.  
PF 26-MAY-1989; 109540.  
PR 27-MAY-1988; US-198915.  
PR 31-AUG-1988; US-238171.  
PR 31-AUG-1988; US-238713.  
PR 23-SEP-1988; US-248521.  
PR 03-NOV-1988; US-266531.  
PA (SYNE-) SYNERGEN INC.  
PI Hannum CH, Eisenberg SP, Thompson RC, Arend WP, Joslin FG,  
PI Sommer A;  
DR WPI; 89-349765/48.  
DR N-PSDB; N92443.  
PT Purified interleukin-1 inhibitor - used as an immuno-suppressing  
PT agent or to prevent tissue destruction at sites of inflammation  
PS Disclosure; Fig 14; 53pp; English.  
CC The inventors specifically claim recombinant DNA molecule GT10-IL1i-  
CC 2A; and the interleukin-1 inhibitors IL-1i-X, IL-1i-alpha and IL-1i-  
CC beta. The preferred component is cDNA or a genomic polynucleotide  
CC sequence. It includes bases 99-557 of GT10-IL1i-2A (see N92441-  
CC N92443). Also claimed is a purified interleukin-1 inhibitor (IL-1i),  
CC which is active against 1 or more than 1 of IL-lalpha and IL-lbeta.  
SQ Sequence 177 AA;

Query Match 87.1%; Score 1130; DB 3; Length 177;  
Best Local Similarity 99.4%; Pred. No. 7.64e-109;  
Matches 155; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 22 eticppsgkrskmqafriwvndqktfyrlnnqlvagylqgpnvnleekidvvpiephal 81  
|  
QY 25 ETICRPSGRKSKMQAFRIWVNDQKTFYLRNQLVAGYLGQPNVNLEEKIDVVPTEPHAL 84  
|  
Db 82 flghgkmcslscvksgetrlqlavnitdlseknrkqkfafirsdgpttsfesaac 141  
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QY 85 FLGHGKMKCLSCVKSGETRLQLEAVNITDLSENKQDKRFNIRSDSGPTTSFSAAC 144  
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Db 142 pgwflctameadqpsltnmpdegvmvtkfyfgede 177  
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QY 145 PGWFLCTAMEADQPSVLTNMPDEGMVMTKFFQDE 180

Search completed: Thu Feb 19 10:09:49 1998  
Job time : 30 secs.

\*\*\*\*\*  
M P S R C H  
\*\*\*\*\* (TM)

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MPsrch\_nnn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Thu Feb 19 09:59:47 1998; MasPar time 82.65 Seconds  
808.366 Million cell updates/sec

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Title: >US-08-910-733-12  
Description: (1-579) from US08910733.seq  
Perfect Score: 579  
N.A. Sequence: 1 CAGAAGGACCTCTCTGCCTA.....TCCAGGAGGACGAGTAGTAC 579  
Comp: GTCTTCTCTGAGGACAGGAT.....AGGTCTCTCTGCTCATCATG

Scoring table: TABLE default  
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 159651 seqs, 57698962 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: n-genes30  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22 23:part23  
24:part24 25:part25 26:part26 27:part27 28:part28  
29:part29 30:part30 31:part31 32:part32 33:part33

Statistics: Mean 8.641; Variance 5.257; scale 1.644

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES					% Match		Query		Pred. No.	
Result No.	Score	Match	Length	ID	Description					
1	579	100.0	579	22	T15099	Intracellular IL-1 re	0.00e+00			
2	474	81.9	589	15	Q90813	Human IL-1 receptor a	0.00e+00			
3	474	81.9	611	3	Q14843	Variant IL-1 cytokine	0.00e+00			
4	472	81.5	540	3	N92441	Sequence of bps 61-60	0.00e+00			
5	472	81.5	600	7	Q40753	GT10-IL-11-2A fragmen	0.00e+00			
6	472	81.5	600	3	N92443	Sequence of GT10-IL1i	0.00e+00			
7	469	81.0	532	3	Q14693	IRAP gene.	6.79e-302			
8	468	80.8	531	21	T30157	Interleukin-1 recepto	3.42e-301			
9	467	80.7	557	15	Q89792	IL-1ra gene.	1.72e-300			
10	467	80.7	602	15	Q89793	ICIL-1ra gene.	1.72e-300			
11	466	80.5	531	22	T35255	Human interleukin-1 r	8.64e-300			
12	466	80.5	531	21	T30159	Interleukin-1 recepto	8.64e-300			
13	464	80.1	531	21	T30158	Interleukin-1 recepto	2.19e-298			
14	464	80.1	531	22	T35256	Human interleukin-1 r	2.19e-298			
15	460	79.4	531	22	T13177	Human interleukin-1 r	1.40e-295			

16	456	78.8	456	7	Q40754	IL-1 inhibitor (IL-1i	8.92e-293
17	454	78.4	514	30	T72210	DNA encoding leaderle	2.25e-291
18	454	78.4	514	13	Q83763	Plasmid i5424.	2.25e-291
19	453	78.2	717	13	T72209	DNA encoding interleu	1.13e-290
20	453	78.2	717	13	Q83762	IL1 receptor-antagoni	1.13e-290
21	186	32.1	270	7	Q40752	Lambda GT10-IL-11-2A,	3.51e-105
22	186	32.1	270	3	N92442	Sequence of part of t	3.51e-105
23	55	9.5	1047	2	Q10572	Human Natriuretic Pep	1.30e-18
24	51	8.8	1047	2	Q10572	Human Natriuretic Pep	1.30e-18
25	43	7.4	91	9	Q51746	Oligonucleotide probe	1.95e-11
26	40	6.9	58	2	Q11920	Sequence encoding fir	1.06e-09
27	39	6.7	204	1	N81164	Base substituted E.co	3.94e-09
28	38	6.6	204	1	N81164	Base substituted E.co	1.45e-08
29	37	6.4	91	9	Q51746	Oligonucleotide probe	5.33e-08
30	34	5.9	114	12	Q70467	Generic DNA sequence	2.47e-06
31	34	5.9	114	12	Q70468	Generic DNA sequence	2.47e-06
32	33	5.7	114	12	Q70471	Generic DNA sequence	8.71e-06
33	32	5.5	114	12	Q70465	Generic DNA sequence	3.03e-05
34	32	5.5	986	1	N82421	Sequence of human per	3.03e-05
35	32	5.5	1497	10	Q38462	IL-1 beta gene.	3.03e-05
36	31	5.4	114	12	Q70469	Generic DNA sequence	1.04e-04
37	31	5.4	178	31	T76405	Human endothelin-1 an	1.04e-04
38	31	5.4	460	2	N60284	Sequence encoding new	1.04e-04
39	31	5.4	1750	1	N80433	Bovine interleukin-1	1.04e-04
40	30	5.2	469	30	T72208	DNA encoding human in	3.53e-04
41	30	5.2	478	13	Q83760	Plasmid pDM15449.	3.53e-04
42	30	5.2	579	2	N60285	Sequence encoding new	3.53e-04
43	30	5.2	702	30	T82205	DNA encoding mature h	3.53e-04
44	30	5.2	702	13	Q83758	Plasmid 16963	3.53e-04
45	30	5.2	1507	3	N50060	Sequence encoding int	3.53e-04

ALIGNMENTS

RESULT 1

ID T15099 standard; cDNA; 579 BP.

AC T15099;

DT 22-OCT-1996 (first entry)

DE Intracellular IL-1 receptor antagonist type II.

KW Intracellular IL-1 receptor antagonist; icIL-1ra;

KW secreted IL-1 receptor antagonist; sIL-1ra;

KW interleukin; IL-1a; IL-1B; auto-immune disease; ss.

OS Homo sapiens.

FT Key Location/Qualifiers

FT CDS 34..576

FT /tag= a

PN W09612022-A1.

PD 25-APR-1996.

PF 12-OCT-1995; E04023.

PR 13-OCT-1994; IT-MI2097.

PA (ISTF ) ARS APPLIED RES SYST HOLDING NV.

PI Colotta F, Mantovani A, Muzio M;

DR WPI; 96-222008/22.

DR P-PSDB; R91361.

PT IL-1 receptor antagonist active against IL-1a and -1B - for

PT treating, preventing or diagnosing auto-immune diseases

PS Claim 5: Page 22-23; 36pp; English.

CC An new IL-1 receptor antagonist includes the sequence given in R91360.

CC The complete icIL-1ra1 is given in T15099. The protein is

CC expressed by DNA similar to that encoding the known receptor

CC inhibitor icIL-1ra, but having a 63 bp insert between the first

CC icIL-1ra specific exon and the internal acceptor site of the first

CC exon of sIL-1ra.

SQ Sequence 579 BP; 157 A; 146 C; 155 G; 121 T;

Query Match 100.0%; Score 579; DB 22; Length 579;

Best Local Similarity 100.0%; Pred. No. 0.00e+00;

Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dn 1 cagaagacacctctctatgagccctcccccctgactgtatgataagaa 60

Qy 1 CAGAAGGACCTCTCTATGAGCCCTCCCTAGCTGCTTATGATGAAGA 60



[illegible]

RESULT	
ID	Q90813 standard; cDNA; 589 BP.
AC	Q90813;
DE	02-FEB-1996 (first entry)
DT	Human IL-1 receptor antagonist cDNA.
DE	IL-1 receptor antagonist; IL-1; IL-3; IL-4; IL-10; human;
KW	tumour necrosis factor alpha; moloney murine leukaemia virus;
KW	rheumatoid arthritis; systemic lupus erythematosus; osteoporosis;
KW	osteogenesis imperfecta; Sjorgen's syndrome; systemic sclerosis;
KW	psoyositis-dermatomyositis; vasculitis syndrome; psoratic arthritis;
KW	ankylosing spondylitis; Paget's disease; inflammatory bowel disease;
KW	synovocyte; keratinocyte; chondrocyte; polymorphonuclear leukocyte; ds.
OS	Homo sapiens.
FF	Key
FF	Location/Qualifiers
FT	CDS
FT	14..548
FT	/tag= a
FT	/product= IL-1 receptor antagonist
PN	WO9516353-A1.
PD	22-JUN-1995.
PF	12-DEC-1994; U14337.
PP	14-DEC-1993; US-167642.
PPA	(UIPI-) UNIV PITTSBURGH.
PT	EVANS CH, Robbins PD;
PT	MPL-95-231292/30
DR	P-PSDB: R75784.
PT	Systemic gene therapy of connective tissue diseases, e.g. rheumatoid
PT	arthritis - using viral vectors to deliver nucleotide sequences
PT	encoding therapeutic peptides/proteins esp. IL-1 receptor antagonist
PT	protein
PC	Example 6; Page 44; 68pp; English.
CC	This sequence represents the cDNA for interleukin-1 receptor antagonist
CC	protein (IRAP). The protein encoded by this sequence is a product of
CC	activated macrophages. The protein is also produced in synoviocytes,
CC	keratinocytes, chondrocytes and polymorphonuclear leukocytes. IRAP is a
CC	weak inhibitor of the biological activities of IL-1. IRAP production is
CC	increased by a variety of cytokines and other stimuli including IL-1,

[illegible]

RESULT	3	
ID	Q14843	standard; cDNA; 611 BP.
AC	Q14843;	
DD	13-FEB-1992	(first entry)
DE	Variant IL-1 cytokine inhibitor gene.	
DT	Intracellular; Interleukin-1; cancer;	immunosuppressive; ss.
OS	Homo sapiens.	
Key	Location/Qualifiers	
FFH	Key	
FFT	123..602	
FT	/*tag= a	
FPN	W09117249-A.	
PPD	14-NOV-1991.	
PPF	10-APR-1991; U02460.	
PPR	01-MAY-1990; US-517276.	
PPS	(CETU ) CETUS CORP.	
PPA	(UYNC-) UNIV NORTH CAROLINA.	
PPD	Haskill JS, Martin G.	
PPI	WPI; 91-353770/48.	
PPS	P-PSDB; R15262.	
PPR	New Interleukin-1 antagonists -	used to diagnose conditions

PT mediated by IL-1 and to treat and prevent sepsis and cancer  
 PS Claim 1; Fig 2; 42pp; English.  
 CC The sequence is that encoding an intracellular protein having  
 CC cytokine inhibitory activity, it is a variant interleukin-1 (IL-1)  
 CC of copies of the inhibitor gene present per cell in various types  
 CC of cancers and so measure the degree of overamplification. The  
 CC inhibitor can be administered to patients at high risk of  
 CC developing sepsis or who have already developed it. It may also  
 CC have immunosuppressive effects against rheumatoid arthritis. See  
 CC also Q14844.  
 SQ Sequence 611 BP; 153 A; 166 C; 160 G; 132 T;

Query Match 81.98; Score 474; DB 3; Length 611;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 132 gagacatctccgacccctctggagaaatccagcaagatgcagccttcagaatctgg 191  
 QY 106 GAGACATCTGCCGACCTCTGGAGAAATCCAGCAAGATGCAAGCTTCAGAACTCGG 165  
 Db 192 gatgttaaccagaagacccctctctgagaaacacacactagttgctggatcttgcac 251  
 QY 166 GATGTTAACAGAGACCTTCTATCTGAGGACACACCACTAGTTGCTGGATCTTCAA 225  
 Db 252 gaacaaatgtcaatttagaagaaagatagtggtgtacccattgagcctcatgctctg 311  
 QY 226 GGACCAATGTCAATTAGAAAGAAAGATAGTGTGTACCCATTGAGCCTCATGCTCTG 285  
 Db 312 tctctgggaatccatggagggaagatgctgtcctgtgtcgaagtgtggtgagacc 371  
 QY 286 TCTCTGGGAATCATGGAGGGAAGATGCTGCTGTCTGTCTCAAGTCTGATGATGAGACC 345  
 Db 372 agactccagctggagcagtttaacatcactgacctgagcgagacagacagcagacaag 431  
 QY 346 AGACTCCAGCTGGAGCGAGTTACATCATTGACTGAGCGGACACACAGAGCAGACAAG 405  
 Db 432 cgcttcgcttcctccgctcagacagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 491  
 QY 406 CGCTTCGCTTCATCGCTCAGACAGTGGCGCCGCCACCACTAGTTTGTAGTCTGCGCCTGC 465  
 Db 492 cccggtgttctctgcacagcgatggaagatgacacagcccgctcagcctcaccacatg 551  
 QY 466 CCGGTTGTTCTCTGACAGCGGATGGAAGCTGACAGCCCGCTCAGCCCTCACCAATATG 525  
 Db 552 cctgacgaagggctcagtggtccacaaattctacttccagagcagcagtagtac 605  
 QY 526 CTGACGAGGCGTATGTTACCAAAATTTACTTCTCCAGGAGGACGAGTAGTAC 579

RESULT 4  
 ID N92441 standard; DNA; 540 BP.  
 AC N92441.  
 DT 14-MAR-1992 (first entry)  
 DE Sequence of bps 61-600 of interleukin-1 inhibitor (IL-1) gene.  
 KW Interleukin-1 inhibitor; inflammation therapy;  
 KW immunosuppressive agent; inflamed joint; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 1..497  
 FT /tag= a  
 FT /codon\_start= 3  
 FT EP-343684-A.  
 PD 29-NOV-1989.  
 PF 26-MAY-1989; 109540.  
 PR 27-MAY-1988; US-199915.  
 PR 31-AUG-1988; US-238171.  
 PR 31-AUG-1988; US-238713.  
 PR 23-SEP-1988; US-248521.  
 PR 03-NOV-1988; US-266531.  
 PA (SYNE-) SYNERGEN INC.  
 PI Hannum CH, Eisenberg SP, Thompson RC, Arend WP, Joslin FG,  
 PI Sommer A;

DR WPI: 89-349765/48.  
 DR P-PSDS; P93616.  
 PT Purified interleukin-1 inhibitor - used as an immuno-suppressing  
 PS agent or to prevent tissue destruction at sites of inflammation  
 PS Claim 18; Page 28; 53pp; English.  
 CC The inventors specifically claim recombinant DNA molecule G710-IL1i-  
 CC 2A; and the interleukin-1 inhibitors IL-1i-X, IL-1i-alpha and IL-1i-  
 CC beta. The preferred component is cDNA or a genomic polynucleotide  
 CC sequence. It includes bases 99-557 of G710-IL1i-2A (see N92441-  
 CC N92443). Also claimed is a purified interleukin-1 inhibitor (IL-1i),  
 CC which is active against 1 or more than 1 of IL-1alpha and IL-1beta.  
 SQ Sequence 540 BP; 135 A; 150 C; 132 G; 123 T;  
 Query Match 81.5%; Score 472; DB 3; Length 540;  
 Best Local Similarity 99.8%; Pred. No. 0.00e+00;  
 Matches 473; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Db 27 gagacatctccacccctctggagaaatccagcaagatgcagccttcagaatctgg 86  
 QY 106 GAGACATCTGCCGACCTCTGGAGAAATCCAGCAAGATGCAAGCTTCAGAACTCGG 165  
 Db 87 gatgttaaccagaagacccctctctgagaaacacacactagttgctggatcttgcac 146  
 QY 166 GATGTTAACAGAGACCTTCTATCTGAGGACACACCACTAGTTGCTGGATCTTCAA 225  
 Db 147 ggacaaatgtcaatttagaagaaagatagtggtgtgtgtgtgtgtgtgtgtgtgtgt 206  
 QY 226 GGACCAATGTCAATTAGAAAGAAAGATAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 285  
 Db 207 tctctgggaatccatggagggaagatgctgtcctgtctgtcgaagtgtgtgtgagacc 266  
 QY 286 TCTCTGGGAATCATGGAGGGAAGATGCTGCTGTCTGTCTGTCTGTCTGTCTGTCTGT 345  
 Db 267 agactccagctggagcagtttaacatcactgacctgagcgagacagacagcagacaag 326  
 QY 346 AGACTCCAGCTGGAGCGAGTTACATCATTGACTGAGCGGACACAGAGCAGACAAG 405  
 Db 327 cgcttcgcttcctccgctcagacagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 386  
 QY 406 CGCTTCGCTTCATCGCTCAGACAGTGGCGCCGCCACCACTAGTTTGTAGTCTGCGCCTGC 465  
 Db 387 cccggtgttctctgcacagcgatggaagatgacacagcccgctcagcctcaccacatg 446  
 QY 466 CCGGTTGTTCTCTGACAGCGATGGAAGCTGACAGCCCGCTCAGCCCTCACCAATATG 525  
 Db 447 cctacgaagcgctcagtggtccacaaattctacttccagagcagcagtagtac 500  
 QY 526 CCGGTTGTTCTCTGACAGCGATGGAAGCTGACAGCCCGCTCAGCCCTCACCAATATG 579

RESULT 5  
 ID Q40753 standard; DNA; 600 BP.  
 AC Q40753.  
 DT 26-AUG-1993 (first entry)  
 DE G710-IL-1i-2A fragment.  
 KW Interleukin-1 inhibitor; immunosuppressive; inflammation; cytokine;  
 KW collagenase; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 24..557  
 FT /tag= a  
 FT sig\_peptide 3..98  
 FT /tag= b  
 FT /note= "encodes 32 amino acid N-terminal to the  
 FT amino terminus of the form of IL-1i known as X"  
 FT sig\_peptide 24..98  
 FT /tag= c  
 FT /note= "claim 33, page 30"  
 FT mat\_peptide 99..554  
 FT /tag= c  
 FT /label= IL-1i  
 FT misc\_feature 349..351  
 FT /tag= d

FT /note= "encodes an N residue that is part of a  
FT consensus N-glycosylation site"  
FT msc.feature 99.101  
FT /tag= e  
FT /note= "encodes a P residue; but no P has been  
FT detected at this position (the N-terminus)  
FT of form X of IL-11; this residue may be  
FT modified in the mature protein"  
FT EP-541920-A.  
PD 19-MAY-1993.  
PD 26-MAY-1989; 109540.  
PR 27-MAY-1988; US-199915.  
PR 31-AUG-1988; US-238713.  
PR 31-AUG-1988; US-238713.  
PR 23-SEP-1988; US-248521.  
PR 03-NOV-1988; US-266531.  
PA (SYND ) SYNERGEN INC.  
PI Arend WP, Eisenberg SP, Hannum CH, Joslin FG, Sommer A;  
PI Thompson RC;  
PI WPI; 93-160536/20.  
DR P-PSDB; R35485.

FT New interleukin-1 inhibiting peptide and DNA - useful as  
FT immunosuppressant for treating auto-immune and other immune  
FT disorders  
PS Disclosure: Fig 14: 55pp; English.  
CC A plaque, GT10-IL-11-2A, was isolated from a GT10 library, using  
CC the probes given in Q40757-61.  
CC IL-11 is useful as an immunosuppressive agent. When applied  
CC locally it can be used to prevent tissue destruction in an inflamed  
CC joint and other inflammation sites. This protective effect may be  
CC improved if IL-11 is given with collagenase inhibitors.  
CC Sequence 600 BP; 152 A; 167 C; 147 G; 134 T;

Query Match 81.5%; Score 472; DB 7; Length 600;  
Best Local Similarity 99.8%; Pred. No. 0.00e+00;  
Matches 473; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 87 gagacgatctgccaccctctgagagaaatccagcaagatgcagccttcagaatctgg 146  
QY 106 GAGACGATCTGCCACCTCTGGGAGAAAATCCAGCAAGATGCAAGCCTTCAGAATCTGG 165  
Db 147 gatgttaaccagagacctctctatctaggaacaacaaactagttggtgatactgcaa 206  
QY 166 GATGTTAACCAAGACCTTCTATCTGAGGAACAACCAACTAGTGTGCGATCTTGCAA 225  
Db 207 ggacccaatgtcaatttagaagaagaatagatgtgtaccattgagcctcatgctctg 266  
QY 226 GGACCAATGTCAATTTAGAAGAAAAGATAGATGTGTACCCATTGAGCCTCATGCTCG 285  
Db 267 ttcttggaatccatgagggagagatgctgtctgtgtcaagtctggtgagacc 326  
QY 286 TTCTTGGGAATCCATGTGAGGGAGAGATGCTGCTGTCTGTCAAGTCTGTGATGAGACC 345  
Db 327 agactccagctgagggcagttacatcactgacacacacacacacacagagagagagag 386  
QY 346 AGACTCCAGCTGGAGGAGGAGTTAATCCTGACCTGACCGAGAGACAGAGAGAGAGAG 405  
Db 387 cgcttcgcttcacccctcagacagtggtggcccccaccacacacacacacacacacac 446  
QY 406 CGCTTCGCTTCATCCGCTCAGACAGTGGCCCCACCCACCCAGTTTGTAGTCTGCCGCTGC 465  
Db 447 cccggttggttctctcagacagatggaagctgaccagcccgctcagcctcaccacatg 506  
QY 466 CCGGTTGGTTCTCTGACACAGGATGGAAGCTGACCCGCGCTCAGCCTCACCACATATG 525  
Db 507 cctgagagagcgtcatggttcacacaaattctacttccagagagagagagagtagtac 560  
QY 526 CCTGACGAGGCGCTCATGGTTCACCAATTTCTACTTCCAGGAGGAGGAGTAGTAC 579

RESULT 6  
ID N92443 standard; cDNA; 600 BP.  
AC N92443;  
DT 14-MAR-1992 (first entry)

DE Sequence of GT10-IL11-2A encoding interleukin-1 inhibitor (IL-11).  
KW Interleukin-1 inhibitor; inflammation; inflammation therapy;  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 24..557  
FT /tag= a  
PN EP-343684-A.  
PD 29-NOV-1989.  
PD 26-MAY-1989; 109540.  
PR 27-MAY-1988; US-199915.  
PR 31-AUG-1988; US-238713.  
PR 31-AUG-1988; US-238713.  
PR 23-SEP-1988; US-248521.  
PR 03-NOV-1988; US-266531.  
PA (SYNE-) SYNERGEN INC.  
PI Hannum CH, Eisenberg SP, Thompson RC, Arend WP, Joslin FG,  
PI Sommer A;  
PI WPI; 89-349765/48.  
DR P-PSDB; P96159.

FT Purified interleukin-1 inhibitor - used as an immuno-suppressing  
FT agent or to prevent tissue destruction at sites of inflammation  
PS Disclosure: Fig 14: 53pp; English.  
CC The inventors specifically claim recombinant DNA molecule GT10-IL11-  
CC 2A; and the interleukin-1 inhibitors IL-11-X, IL-11-alpha and IL-11-  
CC beta. The preferred component is cDNA or a genomic polynucleotide  
CC sequence. It includes bases 99-557 of GT10-IL11-2A (see N92441-  
CC N92443). Also claimed is a purified interleukin-1 inhibitor (IL-11),  
CC which is active against 1 or more than 1 of IL-1alpha and IL-1beta.  
CC Sequence 600 BP; 152 A; 167 C; 147 G; 134 T;

Query Match 81.5%; Score 472; DB 3; Length 600;  
Best Local Similarity 99.8%; Pred. No. 0.00e+00;  
Matches 473; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 87 gagacgatctgccaccctctgagagaaatccagcaagatgcagccttcagaatctgg 146  
QY 106 GAGACGATCTGCCACCTCTGGGAGAAAATCCAGCAAGATGCAAGCCTTCAGAATCTGG 165  
Db 147 gatgttaaccagagacctctctatctaggaacaacaaactagttggtgatactgcaa 206  
QY 166 GATGTTAACCAAGACCTTCTATCTGAGGAACAACCAACTAGTGTGCGATCTTGCAA 225  
Db 207 ggacccaatgtcaatttagaagaagaatagatgtgtaccattgagcctcatgctctg 266  
QY 226 GGACCAATGTCAATTTAGAAGAAAAGATAGATGTGTACCCATTGAGCCTCATGCTCG 285  
Db 267 ttcttggaatccatgagggagagatgctgtctgtgtcaagtctggtgagacc 326  
QY 286 TTCTTGGGAATCCATGTGAGGGAGAGATGCTGCTGTCTGTCAAGTCTGTGATGAGACC 345  
Db 327 agactccagctgagggcagttacatcactgacacacacacacacacagagagagagag 386  
QY 346 AGACTCCAGCTGGAGGAGGAGTTAATCCTGACCTGACCGAGAGAGAGAGAGAGAGAG 405  
Db 387 cgcttcgcttcacccctcagacagtggtggcccccaccacacacacacacacacacac 446  
QY 406 CGCTTCGCTTCATCCGCTCAGACAGTGGCCCCACCCACCCAGTTTGTAGTCTGCCGCTGC 465  
Db 447 cccggttggttctctcagacagatggaagctgaccagcccgctcagcctcaccacatg 506  
QY 466 CCGGTTGGTTCTCTGACACAGGATGGAAGCTGACCCGCGCTCAGCCTCACCACATATG 525  
Db 507 cctgagagagcgtcatggttcacacaaattctacttccagagagagagagagtagtac 560  
QY 526 CCTGACGAGGCGCTCATGGTTCACCAATTTCTACTTCCAGGAGGAGGAGTAGTAC 579

RESULT 7  
ID Q14693 standard; DNA; 532 BP.  
AC Q14693;  
DT 17-FEB-1992 (first entry)  
DE IRAP gene.

KW Scavo peptide; IRAP; MIRAP; Interleukin; receptor; inhibitor; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT sig\_peptide 1..75  
 FT /\*tag= a  
 FT mat\_peptide 76..531  
 FT /\*tag= b  
 PN WO9117184-A.  
 PD 14-NOV-1991.  
 PF 03-APR-1991; U02127.  
 PR 27-APR-1990; US-515468.  
 PA (UFOJ ) UFOJOH CO.  
 PI Carter DB;  
 DR WPI; 91-353724/48.  
 DR P-PSDB; RI4400.  
 PT New DNA molecules are modified Interleukin-1 inhibitors -  
 PT comprising an IL-1 receptor antagonist protein and a scavo  
 PT protein, useful for treating arthritis  
 PS Disclosure: Page 25; 29pp; English.  
 CC Probe DC-166 (see Q14694) was used to screen a U937 cDNA library.  
 CC A clone (P5) was isolated and sequenced. The human DNA sequence  
 CC contains ca. 1782 nucleotides including 5' and 3' nontranslated  
 CC sequences. The longest ORF begins with nucleotide 53 (1 in this  
 CC sequence) and extends to nucleotide 584 (532 in this sequence).  
 CC The sequence is used to produce modified IRAP by addition of  
 CC Scavo peptides.  
 CC See also Q14690-4.  
 SQ Sequence 532 BP; 138 A; 147 C; 129 G; 118 T;  
 Query Match 81.0%; Score 469; DB 3; Length 532;  
 Best Local Similarity 100.0%; Pred. No. 6,79e-302;  
 Matches 469; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 64 gagacgatctgcgacccctctggagagaaatccagcaagatgcaagccttcagaatctgg 123  
 QY 106 GAGACGATCTGCGACCCCTCTGGAGAAATCCAGCAAGATGCAAGCCTTCAGAACTGG 165  
 Db 124 gatgttaaccagaagaccctctctatctaggagaaacacaaactagttgtgatacttgcaa 183  
 QY 166 GATGTTAACCAAGACCTTCTATCTGAGAAAGATAGATGTGTGATGCTGCTGCTG 225  
 Db 184 ggacaaatgtcaatttagaagaaagatagatgtgtgtacccattgagcctcatgctcg 243  
 QY 226 GGACCAATGTCAATTAGAAAGAAAGATAGATGTGTGATGCTGCTGCTGCTG 285  
 Db 244 tcttgggaatccatggaggagatgtgcctgtcctgtgtcaagtctggtgatgagacc 303  
 QY 286 TTCTTGGGAATCCATGGAGGAGATGTGCTGTCTGTCTCAAGTCTGGTGTGAGACC 345  
 Db 304 agactccagctggaggcagtttaacatcactgacctgagcgagagaaagcaggagcaag 363  
 QY 346 AGACTCCAGCTGGAGCAGTTAAATCACTGACCTGAGCGAGAGCAAGAGGAGCAAG 405  
 Db 364 cgttcgcttcaatccgttcagacagatggccccaccacagttttgagtcgcgcctgc 423  
 QY 406 CGCTTCGCCTTATCCGCTCAGACAGTGGCCCCACCACAGTTTGTGAGTCTGCGCCTGC 465  
 Db 424 ccggttggttctctgcacagcagatggagctgacccagcctcagcctcaccatag 483  
 QY 466 CCGGTGTGTTCTCTGACAGCGATGGAGCTGACAGCCCGTCCAGCTTCACCAATATG 525  
 Db 484 cctgacgaaggcgtcatggtccacaaattctacttccaggagagcaggt 532  
 QY 526 CCTGACGAAGGGTCTATGTCACCAATTTCTACTTCCAGGAGGACGAGT 574

RESULT 8  
 ID T30157 standard; DNA; 531 BP.  
 AC T30157;  
 DT 23-SEP-1996 (first entry)  
 DE Interleukin-1 receptor antagonist cDNA.  
 KW Drug delivery; Escherichia coli; Bacillus subtilis;  
 Lactobacillus; Interleukin-1 receptor antagonist; IL-1ra;

KW septic shock; therapy; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT sig\_peptide 1..75  
 FT /\*tag= a  
 FT mat\_peptide 76..531  
 FT /\*tag= b  
 PN WO9611277-A1.  
 PD 18-APR-1996.  
 PF 04-OCT-1995; E03921.  
 PR 05-OCT-1994; IT-MI2025.  
 PA (DOMP-) DOME SPA.  
 PI Boraschi D, Bossu P, Macchia G, Maurizi G, Porzio S;  
 PI Ruggiero P, Tagliabue A;  
 DR WPI; 96-209858/21.  
 DR P-PSDB; R98251.  
 PT Engineered microorganisms expressing therapeutic proteins - useful  
 PT as therapeutic delivery systems for the treatment of disease.  
 PS Disclosure: Fig 4; 77pp; English.  
 CC A cDNA clone (T30157) codes for human interleukin-1 receptor  
 CC antagonist (IL-1ra) (R98251), a protein that is structurally  
 CC similar to IL-1 and which binds with high affinity to the IL-1  
 CC receptor but does not activate target cells. It has potential as  
 CC a therapeutic agent for the treatment of inflammatory and  
 CC matrix-destruction diseases e.g. septic shock. The cDNA or clones  
 CC (see also T30158-59) coding for IL-1ra mutants (R98252-53) can be  
 CC inserted into a vector to allow expression in Bacillus subtilis  
 CC transformants. In vivo administration of these transformants  
 CC results in detectable plasma levels of IL-1ra, demonstrating trans-  
 CC mucosal absorption of a recombinant therapeutic protein produced by  
 CC a microbial host.  
 SQ Sequence 531 BP; 138 A; 147 C; 129 G; 117 T;  
 Query Match 80.8%; Score 468; DB 21; Length 531;  
 Best Local Similarity 100.0%; Pred. No. 3.42e-301;  
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 64 gagacgatctgcgacccctctggagagaaatccagcaagatgcaagccttcagaatctgg 123  
 QY 106 GAGACGATCTGCGACCCCTCTGGAGAAATCCAGCAAGATGCAAGCCTTCAGAACTGG 165  
 Db 124 gatgttaaccagaagaccctctctatctaggagaaacacaaactagttgtgatacttgcaa 183  
 QY 166 GATGTTAACCAAGACCTTCTATCTGAGAAAGATAGATGTGTGATGCTGCTGCTG 225  
 Db 184 ggacaaatgtcaatttagaagaaagatagatgtgtgtacccattgagcctcatgctcg 243  
 QY 226 GGACCAATGTCAATTAGAAAGAAAGATAGATGTGTGATGCTGCTGCTGCTG 285  
 Db 244 tcttgggaatccatggaggagatgtgcctgtcctgtgtcaagtctggtgatgagacc 303  
 QY 286 TTCTTGGGAATCCATGGAGGAGATGTGCTGTCTGTCTCAAGTCTGGTGTGAGACC 345  
 Db 304 agactccagctggaggcagtttaacatcactgacctgagcgagagaaagcaggagcaag 363  
 QY 346 AGACTCCAGCTGGAGCAGTTAAATCACTGACCTGAGCGAGAGCAAGAGGAGCAAG 405  
 Db 364 cgttcgcttcaatccgttcagacagatggccccaccacagttttgagtcgcgcctgc 423  
 QY 406 CGCTTCGCCTTATCCGCTCAGACAGTGGCCCCACCACAGTTTGTGAGTCTGCGCCTGC 465  
 Db 424 ccggttggttctctgcacagcagatggagctgacccagcctcagcctcaccatag 483  
 QY 466 CCGGTGTGTTCTCTGACAGCGATGGAGCTGACAGCCCGTCCAGCTTCACCAATATG 525  
 Db 484 cctgacgaaggcgtcatggtccacaaattctacttccaggagagcaggt 531  
 QY 526 CCTGACGAAGGGTCTATGTCACCAATTTCTACTTCCAGGAGGACGAGT 573

RESULT 9  
 ID Q89792 standard; DNA; 557 BP.  
 AC Q89792;

28-NOV-1995 (first entry)  
 IL-lra gene.  
 Interleukin-1; receptor antagonist; ovulation prevention; embryo;  
 Implantation; contraceptive; ss.  
 Homo sapiens.  
 Key Location/Qualifiers  
 CDS 24..557  
 FT /\*tag= a  
 PN W09510298-A.  
 PD 20-APR-1995.  
 PF 12-OCT-1994; U11588.  
 PR 12-OCT-1993; US-136077.  
 PA (POLA/) POLAN M L.  
 PA (POLA/) POLAN M.  
 PA (SIMO/) SIMON C.  
 PI Polan ML, Simon C, Polan M;  
 DR WPI; 95-169961/22.  
 DR P-PSDB; R73641.  
 PT Method of ovulation using interleukin-1 receptor antagonist -  
 prevents ovulation and implantation of embryo, also contraceptive  
 device comprising the antagonist  
 PS Disclosure; Fig 6; 59pp; English.  
 CC The sequence is that of the gene encoding IL-lra, an interleukin-1  
 receptor antagonist. The gene and its product can be used in a  
 composition (claimed) to prevent ovulation and implantation of an  
 embryo in a mammalian uterus. The IL-1 receptor antagonist is  
 useful in contraceptive compns. It is also useful after the  
 fertilisation event and provide an alternative to known means of  
 terminating pregnancy post-fertilisation.  
 CC See also Q89793.  
 SQ Sequence 557 BP; 147 A; 153 C; 135 G; 122 T;  
 Query Match 80.7%; Score 467; DB 15; Length 557;  
 Best Local Similarity 99.6%; Pred. No. 1.72e-300;  
 Matches 469; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

87 gagacatctgcgagccctctggagaaaatccagcaagatgagccttcagaattctg 146  
 |||||  
 QY 106 GAGACATCTGCCGACCCCTCTGGGAGAAAATCCAGCAAGATGCAAGCTTCAGAAATCTGG 165  
 |||||  
 Db 147 gatgttaacagagacctctctctgaggaacacacactagttgctgatacttcaa 206  
 |||||  
 QY 166 GATGTTAACAGAGACCTCTATCTGAGGAACAACTAGTTGCTGGATCTGCAA 225  
 |||||  
 Db 207 ggaccaaattgcaatttagaagaaaagatagatgtgtaccattgagcctcatgctctg 266  
 |||||  
 QY 226 GGACCAAATGTCATTTAGAGAAAAGATAGATGTGTGTACCCATTGAGCTCATGCTCTG 285  
 |||||  
 Db 267 ttcttgggaatccatggaggaagatgtgctgtctctgtgtcactgtgtgatgagacc 326  
 |||||  
 QY 286 TTCTTGGGAATCCATGGAGGGAAGATGTGCTGTCTGTCTCAAGTCTGGTGATGAGACC 345  
 |||||  
 Db 327 agactccagctggagcagttacatcactgacctgagcagacagacagagcagacaag 386  
 |||||  
 QY 346 AGACTCCAGCTGGAGGAGGTTACATCATTGACCTGAGGAGACAAAGACGAGACAAG 405  
 |||||  
 Db 387 cgcttcgcttcacgctcagacagtggtgcccaccaccagttttagtctgcccgtctg 446  
 |||||  
 QY 406 CGCTTCGCCCTTCATCGCTCAGACAGTGGCCCCACCACCATGTTTGTAGTCTGCCGCTGC 465  
 |||||  
 Db 447 cccggttggctctctgcacagcgatggaagctgaccagcccgtcagcctcacaatg 506  
 |||||  
 QY 466 CCCGGTGTGTTCTCTGACAGGAGTGGAAAGCTGACCAAGCCGCTCAGCCCTCACCATAATG 525  
 |||||  
 Db 507 cctgacgaagggcctcatgttcacaaattctacttccagagagcagtag 557  
 |||||  
 QY 526 CTTGACGAAGGCGTCTATGTTGTCACCAATTTCTACTTCCAGGAGGACGAGTAG 576  
 |||||

RESULT 10  
 ID Q89793 standard; DNA; 602 BP.  
 AC Q89793;  
 DT 28-NOV-1995 (first entry)

ICIL-lra gene.  
 Interleukin-1; receptor antagonist; ovulation prevention; embryo;  
 Implantation; contraceptive; ss.  
 Homo sapiens.  
 Key Location/Qualifiers  
 CDS 123..602  
 FT /\*tag= a  
 PN W09510298-A.  
 PD 20-APR-1995.  
 PF 12-OCT-1994; U11588.  
 PR 12-OCT-1993; US-136077.  
 PA (POLA/) POLAN M L.  
 PA (POLA/) POLAN M.  
 PA (SIMO/) SIMON C.  
 PI Polan ML, Simon C, Polan M;  
 DR WPI; 95-169961/22.  
 DR P-PSDB; R73642.  
 PT Method of ovulation using interleukin-1 receptor antagonist -  
 prevents ovulation and implantation of embryo, also contraceptive  
 device comprising the antagonist  
 PS Disclosure; Fig 7; 59pp; English.  
 CC The sequence is that of the gene encoding ICIL-lra, an interleukin-1  
 receptor antagonist. The gene and its product can be used in a  
 composition (claimed) to prevent ovulation and implantation of an  
 embryo in a mammalian uterus. The IL-1 receptor antagonist is  
 useful in contraceptive compns. It is also useful after the  
 fertilisation event and provide an alternative to known means of  
 terminating pregnancy post-fertilisation.  
 CC See also Q89792.  
 SQ Sequence 602 BP; 151 A; 164 C; 157 G; 130 T;  
 Query Match 80.7%; Score 467; DB 15; Length 602;  
 Best Local Similarity 99.6%; Pred. No. 1.72e-300;  
 Matches 469; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

132 gagacatctgcgagccctctggagaaaatccagcaagatgagccttcagaattctg 191  
 |||||  
 QY 106 GAGACATCTGCCGACCCCTCTGGGAGAAAATCCAGCAAGATGCAAGCTTCAGAAATCTGG 165  
 |||||  
 Db 192 gatgttaacagagacctctctctgaggaacacacactagttgctgatacttcaa 251  
 |||||  
 QY 166 GATGTTAACAGAGACCTCTATCTGAGGAACAACTAGTTGCTGGATCTGCAA 225  
 |||||  
 Db 252 ggaccaaattgcaatttagaagaaaagatagatgtgtaccattgagcctcatgctctg 311  
 |||||  
 QY 226 GGACCAAATGTCATTTAGAGAAAAGATAGATGTGTGTACCCATTGAGCTCATGCTCTG 285  
 |||||  
 Db 312 ttcttgggaatccatggaggaagatgtgctgtctctgtgtcactgtgtgatgagacc 371  
 |||||  
 QY 286 TTCTTGGGAATCCATGGAGGGAAGATGTGCTGTCTGTCTCAAGTCTGGTGATGAGACC 345  
 |||||  
 Db 372 agactccagctggagcagttacatcactgacctgagcagacagacagagcagacaag 431  
 |||||  
 QY 346 AGACTCCAGCTGGAGGAGGTTACATCATTGACCTGAGGAGACAAAGACGAGACAAG 405  
 |||||  
 Db 432 cgcttcgcttcacgctcagacagtggtgcccaccaccagttttagtctgcccgtctg 491  
 |||||  
 QY 406 CGCTTCGCCCTTCATCGCTCAGACAGTGGCCCCACCACCATGTTTGTAGTCTGCCGCTGC 465  
 |||||  
 Db 492 cccggttggctctctgcacagcgatggaagctgaccagcccgtcagcctcacaatg 551  
 |||||  
 QY 466 CCCGGTGTGTTCTCTGACAGGAGTGGAAAGCTGACCAAGCCGCTCAGCCCTCACCATAATG 525  
 |||||  
 Db 552 cctgacgaagggcctcatgttcacaaattctacttccagagagcagtag 602  
 |||||  
 QY 526 CTTGACGAAGGCGTCTATGTTGTCACCAATTTCTACTTCCAGGAGGACGAGTAG 576  
 |||||

RESULT 11  
 ID T35255 standard; cDNA; 531 BP.  
 AC T35255;  
 DT 06-NOV-1996 (first entry)  
 DE Human interleukin-1 receptor antagonist mutant, MILRA-2, cDNA.

KW Interleukin-1 receptor; antagonist; IL-1; inflammatory disease;  
 KW rheumatoid arthritis; allergy; graft rejection; autoimmune disease;  
 OS recombinant; vector; ds.  
 FH Key Location/Qualifiers  
 FT CDS 1..531  
 FT /tag= a  
 FT /note= "no stop codon"  
 FT sig\_peptide 1..75  
 FT /tag= b  
 FT mat\_peptide 76..531  
 FT /tag= c  
 FT mutation 400..402  
 FT /tag= d  
 FT /note= "ACC to GCC substitution, for the preferred  
 FT Thr to Ala substitution in the mutant IL-1  
 FT receptor antagonist protein"  
 PN WO9609323-A1.  
 PD 28-MAR-1996.  
 PF 20-SEP-1995; E02708.  
 PI 21-SEP-1994; IT-MI1916.  
 PI (DMP-) DOMPE SPA.  
 PI Boraschi D, Bossu P, Frascotti G, Frigerio F, Grandi G;  
 PI Grifantini R, Macchia G, Ruggiero P, Tagliabue A;  
 DR WPI; 96-188402/19.  
 DR P-PSDB; R99262.  
 PT Interleukin-1 receptor antagonist mutants - have enhanced  
 PT inhibitory activity, useful for the treatment of rheumatoid  
 PT arthritis; allergies, graft rejection, etc.  
 PS Claim 1; Page -; 41pp; English.  
 CC T13177, T35255 and T35256 are cDNA sequences encoding mutant  
 CC versions of a human interleukin-1 (IL-1) receptor antagonist  
 CC The sequences encode mutants MILRA-3, MILRA-2 and MILRA-1  
 CC respectively, which contain at least one of the following two  
 CC substitutions: Asn to Arg at position 91 of the mature protein or  
 CC Thr to Ala at position 109 of the mature protein. The IL-1 receptor  
 CC antagonist mutants have an improved capacity for interaction with  
 CC IL-1 receptor type I (largely responsible for cell activation in  
 CC response to IL-1). The mutant proteins can be used in the prepn. of  
 CC drugs capable of antagonising the inflammatory, neurological,  
 CC endocrinological, haematological, metabolic, catabolic and  
 CC immunosuppressant effects associated with IL-1, and in particular for  
 CC the treatment of acute or chronic inflammatory pathologies e.g.  
 CC rheumatoid arthritis.  
 SQ Sequence 531 BP; 137 A; 147 C; 130 G; 117 T;  
 Query Match 80.5%; Score 466; DB 22; Length 531;  
 Best Local Similarity 99.8%; Pred. No. 8.64e-300;  
 Matches 467; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 64 gagacgatctgcgacccctctggagagaaatccagcaagatgcaagccttcagaatctgg 123  
 106 GAGACGATCTGCCGACCCCTCTGGAGAAAATCCAGCAAGATGCAAGCTTCAGAATCTGG 165  
 124 gatgttaaccagaagacccctctatctgaggaacaaacactagttgtgatacttgcga 183  
 166 GATGTTAAACAGAAAGACCTTCTATCTGAGGAACAAACCACTAGTTGCTGATCTGCA 225  
 184 ggaccaaattgcatttagaagaagaatagatgtgtacccattgacctcatgctctg 243  
 226 GGACCAAATGTCAAATTTAGAGAAGAAATAGATGTGTGCTGCTGATGAGACCTG 285  
 244 ttcttgggaatccatgaggaagaatgctgtcctgtgtcctgtgtcctgtgtgagagacc 303  
 286 TTCTTGGGAATCCATGAGGGAAGATGTGCTGTGCTGTGCTGTGCTGTGATGAGACC 345  
 304 agactccagctggaggcaggttaacatacactgacgtgagcgagacagaagcaggacaag 363  
 346 AGACTCCAGCTGGAGGCGAGTATACATCACTGACCTGAGCGAGACAGAAAGCAGACAAG 405  
 364 cgttcgcttcacgcctcagacagtgcccccacgcgcaggttttagtctgcccgtcgc 423  
 406 CGCTTCGCTTCATCCGCTCAGACAGTGGGCCCCACCACCACTGTTTGTGCTGCGCCTGC 465

Db 424 cccggttggttcctctgcacagcgatggaagctgacccagcccgctcagcctcacaatg 483  
 QY |||||||  
 Db 466 CCCGTTGGTTCCCTCTGCACAGCGATGAGAGCTGACCAAGCCGTCAGCCTACCAATG 525  
 QY |||||||  
 Db 484 cctgacgaagcgctcaggtccacaaattctacttccaggaggagag 531  
 QY |||||||  
 QY 526 CTTGACGAAGCGCTGATGGTCCACAAATCTTACTTCCAGGAGGAGCGAG 573  
 |||||||  
 RESULT 12  
 ID T30159 standard; DNA; 531 BP.  
 AC T30159;  
 DT 23-SEP-1996 (first entry)  
 DE Interleukin-1 receptor antagonist mutant T109A cDNA.  
 KW Drug delivery; Escherichia coli; Bacillus subtilis;  
 KW Lactobacillus; interleukin-1 receptor antagonist; IL-1ra;  
 KW septic shock; therapy; ss.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT mutation 400  
 FT /tag= a  
 FT /note= "wild-type base a at position 400 is  
 FT mutated to g, resulting in T109A  
 FT mutation in the mature IL-1ra protein"  
 PN WO9611277-A1.  
 PD 18-APR-1996.  
 PF 04-OCT-1995; E03921.  
 PR 05-OCT-1994; IT-MI2025.  
 PA (DMP-) DOMPE SPA.  
 PI Boraschi D, Bossu P, Macchia G, Maurizi G, Porzio S;  
 PI Ruggiero P, Tagliabue A;  
 DR WPI; 96-209858/21.  
 DR P-PSDB; R98253.  
 PT Engineered microorganisms expressing therapeutic proteins - useful  
 PT as therapeutic delivery systems for the treatment of disease.  
 PS Example 2; Fig 4; 77pp; English.  
 CC A cDNA clone (T30159) codes for human interleukin-1 receptor  
 CC antagonist (IL-1ra) mature protein mutant T109A (R98253). It was  
 CC obtd. by site-directed mutagenesis of cDNA (T30157) coding for  
 CC wild-type IL-1ra (R98251). The mutant retains the activity of  
 CC IL-1ra. cDNAs coding for wild-type or mutant IL-1ra (see also  
 CC T30158) can be inserted into a vector to allow expression in Bacillus  
 CC subtilis transformants. In vivo administration of the transformants  
 CC results in detectable plasma levels of IL-1ra, demonstrating trans-  
 CC mucosal absorption of a recombinant therapeutic protein produced by  
 CC a microbial host.  
 SQ Sequence 531 BP; 137 A; 147 C; 130 G; 117 T;  
 Query Match 80.5%; Score 466; DB 21; Length 531;  
 Best Local Similarity 99.8%; Pred. No. 8.64e-300;  
 Matches 467; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 64 gagacgatctgcgacccctctggagagaaatccagcaagatgcaagccttcagaatctgg 123  
 106 GAGACGATCTGCCGACCCCTCTGGAGAAAATCCAGCAAGATGCAAGCTTCAGAATCTGG 165  
 124 gatgttaaccagaagacccctctatctgaggaacaaacactagttgtgatacttgcga 183  
 166 GATGTTAAACAGAAAGACCTTCTATCTGAGGAACAAACCACTAGTTGCTGATCTGCA 225  
 184 ggaccaaattgcatttagaagaagaatagatgtgtacccattgacctcatgctctg 243  
 226 GGACCAAATGTCAAATTTAGAGAAGAAATAGATGTGTGCTGCTGATGAGACCTG 285  
 244 ttcttgggaatccatgaggaagaatgctgtcctgtgtcctgtgtcctgtgtgagagacc 303  
 286 TTCTTGGGAATCCATGAGGGAAGATGTGCTGTGCTGTGCTGTGCTGTGATGAGACC 345  
 304 agactccagctggaggcaggttaacatacactgacgtgagcgagacagaagcaggacaag 363  
 346 AGACTCCAGCTGGAGGCGAGTATACATCACTGACCTGAGCGAGACAGAAAGCAGACAAG 405  
 364 cgttcgcttcacgcctcagacagtgcccccacgcgcaggttttagtctgcccgtcgc 423  
 406 CGCTTCGCTTCATCCGCTCAGACAGTGGGCCCCACCACCACTGTTTGTGCTGCGCCTGC 465

Db 364 cgccttcgcttcacgctcagacagtgcccccacagcagcttttgagctgcgctgc 423  
 QY 406 CGCTTCGCTTCATCCGCTCAGACAGTGGCCCCACACCACTGAGTTCGCGCCTGC 465  
 Db 424 cccggttggttcctctgcacagcgatgaagctgacagccgctcagctccaccaatag 483  
 QY 466 CCGGTTGGTTCCTCTGCACAGGATGGAGCTGACGAGCCGCTCAGCCTCACCATAATG 525  
 Db 484 cctgcaggaagcgctcatggtccacaaattctacttccagagagcgag 531  
 QY 526 CCGTACGAGGCGTCATGGTCCACAAATCTACTTCCAGGAGGACGAG 573

RESULT 13  
 ID T30158 standard; DNA; 531 BP.  
 AC T30158;  
 DT 23-SEP-1996 (first entry)  
 DE Interleukin-1 receptor antagonist mutant C91R cDNA.  
 KW Drug delivery; Escherichia coli; Bacillus subtilis;  
 KW Lactobacillus; Interleukin-1 receptor antagonist; IL-1ra;  
 KW septic shock; therapy; ss.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT mutation 346..347  
 FT /\*tag= a  
 FT /\*note= "wild-type bases aa at positions 346-347  
 FT are mutated to cg, resulting in C91R  
 FT mutation in the mature IL-1ra protein"  
 PN WO9611277-A1.  
 PD 18-APR-1996.  
 PF 04-OCT-1995; E03921.  
 PF 05-OCT-1994; IT-MI2025.  
 PA (DMP-) DOMPE SPA.  
 PI Boraschi D, Bossu P, Macchia G, Maurizi G, Porzio S;  
 PI Ruggiero P, Tagliabue A;  
 DR WPI: 96-209858/21.  
 DR P-PSDB; R98252.  
 PT Engineered microorganisms expressing therapeutic proteins - useful  
 PT as therapeutic delivery systems for the treatment of disease.  
 PS Example 2; Fig 4; 77pp; English.  
 CC A cDNA clone (T30158) codes for human interleukin-1 receptor  
 CC antagonist (IL-1ra) mature protein mutant C91R (R98252). It was  
 CC obt'd. by site-directed mutagenesis of cDNA (T30157) coding for  
 CC wild-type IL-1ra (R98251). The C91R mutant retains the activity of  
 CC IL-1ra. cDNAs coding for wild-type or mutant IL-1ra (see also  
 CC T30159) can be inserted into a vector to allow expression in Bacillus  
 CC subtilis transformants. In vivo administration of the transformants  
 CC results in detectable plasma levels of IL-1ra, demonstrating trans-  
 CC mucosal absorption of a recombinant therapeutic protein produced by  
 CC a microbial host.  
 SQ Sequence 531 BP; 136 A; 148 C; 130 G; 117 T;

Query Match 80.1%; Score 464; DB 21; Length 531;  
 Best Local Similarity 99.6%; Pred. No. 2.19e-298;  
 Matches 466; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 64 gagacgatctgcgacccctcggagaaaatccagcaagatgcaagccttcagaatctg 123  
 QY 106 GAGACGATCTGGCGACCTCTGGAGAAATCCAGCAAGATGCAAGCCTTCAGAACTGG 165  
 Db 124 gatgttaacagaagacctctctatctgaggaacaacaactagtgtgatacttgcaa 183  
 QY 166 GATGTTAAACAGAAAGACCTTCTATCTGAGGAACAACAACACTAGTTGCTGGTACTTGC 225  
 Db 184 gacacaaatgcaattagaagaagatagatggtgacccattgagcctcagctctg 243  
 QY 226 GGACCAAAATGTAATTTAGAAGAAAAGATAGATGTGGTACCCATTGAGCCTCATGCTCTG 285  
 Db 244 tctctgggaatccatggaggagatgctgctcctgtctgctcaagtctggtgatgagacc 303  
 QY 286 TTTCTGGGAATCCATGGAGGAGATGTGCCTGCTCTGCTGCTCAAGTCTGCTGATGAGACC 345  
 Db 304 agactccagctggaggcagtaacatcatcactgacctgagcgagcgagaaagcaggacaag 363

QY 346 AGACTCAGCTGGAGGAGTAAACATCAGCTGAGCGGAGAACAGAGGACGAG 405  
 Db 364 cgccttcgcttcacgctcagacagtgcccccacagcagcttttgagctgcgctgc 423  
 QY 406 CGCTTCGCTTCATCCGCTCAGACAGTGGCCCCACACCACTGAGTTCGCGCCTGC 465  
 Db 424 cccggttggttcctctgcacagcgatgaagctgacagccgctcagctccaccaatag 483  
 QY 466 CCGGTTGGTTCCTCTGCACAGGATGGAGCTGACGAGCCGCTCAGCCTCACCATAATG 525  
 Db 484 cctgcaggaagcgctcatggtccacaaattctacttccagagagcgag 531  
 QY 526 CCGTACGAGGCGTCATGGTCCACAAATCTACTTCCAGGAGGACGAG 573

RESULT 14  
 ID T35256 standard; cDNA; 531 BP.  
 AC T35256;  
 DT 06-NOV-1996 (first entry)  
 DE Human interleukin-1 receptor antagonist mutant, MILRA-1, cDNA.  
 KW Interleukin-1 receptor; antagonist; IL-1; inflammatory disease;  
 KW rheumatoid arthritis; allergy; graft rejection; autoimmune disease;  
 KW recombinant; vector; ds.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT CDS 1..531  
 FT /\*tag= a  
 FT /\*note= "no stop codon"  
 FT sig\_peptide 1..75  
 FT /\*tag= b  
 FT mat\_peptide 76..531  
 FT /\*tag= c  
 FT mutation 346..348  
 FT /\*tag= d  
 FT /\*note= "AAC to CGC substitution, for the preferred  
 FT Asn to Arg substitution in the mutant IL-1  
 FT receptor antagonist protein"  
 PN WO9609323-A1.  
 PD 28-MAR-1996.  
 PF 20-SEP-1995; E03708.  
 PR 21-SEP-1994; IT-MI1916.  
 PA (DMP-) DOMPE SPA.  
 PI Boraschi D, Bossu P, Frascotti G, Frigerio F, Grandi G;  
 PI Grifantini R, Macchia G, Ruggiero P, Tagliabue A;  
 DR WPI: 96-188402/19.  
 DR P-PSDB; R99263.  
 PT Interleukin-1 receptor antagonist mutants - have enhanced  
 PT inhibitory activity, useful for the treatment of rheumatoid  
 PT arthritis, allergies, graft rejection, etc.  
 PS Claim 1; Page -; 41pp; English.  
 CC T13177, T35255 and T35256 are cDNA sequences encoding mutant  
 CC versions of a human interleukin-1 (IL-1) receptor antagonist protein.  
 CC The sequences encode mutants MILRA-3, MILRA-2 and MILRA-1  
 CC substitively, which contain at least one of the following two  
 CC substitutions: Asn to Arg at position 91 of the mature protein or  
 CC Thr to Ala at position 109 of the mature protein. The IL-1 receptor  
 CC antagonist mutants have an improved capacity for interaction with  
 CC IL-1 receptor type I (largely responsible for cell activation in  
 CC response to IL-1). The mutant proteins can be used in the prepn. of  
 CC drugs capable of antagonising the inflammatory, neurological, and  
 CC endocrinological, haematological, metabolic, catabolic and  
 CC immunostimulant effects associated with IL-1, and in particular for  
 CC the treatment of acute or chronic inflammatory pathologies e.g.  
 CC rheumatoid arthritis.  
 SQ Sequence 531 BP; 136 A; 148 C; 130 G; 117 T;

Query Match 80.1%; Score 464; DB 22; Length 531;  
 Best Local Similarity 99.6%; Pred. No. 2.19e-298;  
 Matches 466; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 64 gagacgatctgcgacccctcggagaaaatccagcaagatgcaagccttcagaatctg 123  
 |||||

QY 106 GAGACGATCTCCGACCTCTGGAGAAATCCAGCAAGATGCAAGCCTTCAGATCTGG 165  
Db 124 gatgttaaccagaagaccttctatctgaggaacaaccaactagttgtggtacttgcaa 183  
QY 166 GATGTTAAACAGAGACCTTCTATCTGAGGAACAACCAACTAGTTGCTGGATCTGCA 225  
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QY 226 GGACCAATGCAATTTAGAGAAAGATAGATGTGTACCCATGAGCCCTCATGCTCTG 285  
Db 244 ttcttggaatccatgaggaagatgctctgctcctgctcctgctcctgctcctgctc 303  
QY 286 TTCTTGGGAATCATTGAGGGAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 345  
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Db 364 cgcttcgcttcacgtcagacagtgagtgagtgagtgagtgagtgagtgagtgagtgag 423  
QY 406 CGCTTCGCTTCATCCGCTCAGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 465  
Db 424 ccggttggttctctcagcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 483  
QY 466 CCCTGAGGAGGCGTCATGGTCAACCAATTTCTACTTCCAGGAGGAGGAGGAGGAGGAG 525

RESULT 15  
ID T13177 standard; cDNA; 531 BP.  
AC T13177;  
DT 06-NOV-1996 (first entry)  
DE Human interleukin-1 receptor antagonist mutant, MILRA-3, cDNA.  
KW Interleukin-1 receptor; antagonist; IL-1; inflammatory disease;  
KW rheumatoid arthritis; allergy; graft rejection; autoimmune disease;  
KW recombinant; vector; ds.  
OS Synthetic.  
FH Key Location/Qualifiers  
FT CDS 1..531  
FT /\*tag= a  
FT /\*note= "no stop codon"  
FT sig\_peptide 1..75  
FT /\*tag= b  
FT mat\_peptide 76..531  
FT /\*tag= c  
FT mutation 346..348  
FT /\*tag= d  
FT /\*note= "AAC to CGC substitution, for the preferred  
FT Asn to Arg substitution in the mutant IL-1  
FT receptor antagonist protein"  
FT mutation 400..402  
FT /\*tag= e  
FT /\*note= "ACC to GCC substitution, for the preferred  
FT Thr to Ala substitution in the mutant IL-1  
FT receptor antagonist protein"  
PN WO9609323-A1.  
PD 28-MAR-1996.  
PF 20-SEP-1995; E03708.  
PR 21-SEP-1994; IT-M11916.  
PA (DMP-) DOME SPA.  
PI Rosaschi, D., Bressan, F., Frascotti G., Frigerio F., Grandi G;  
PI Grifantini R, Macchia G, Ruggiero P, Tagliabue A;  
DR WPI; 96-188402/19.  
DR P-PSDB; R99261.  
PT Interleukin-1 receptor antagonist mutants - have enhanced  
PT inhibitory activity, useful for the treatment of rheumatoid  
PT arthritis, allergies, graft rejection, etc.  
PS Claim 1; Page -; 41pp; English.  
CC T13177, T35255 and T35256 are cDNA sequences encoding mutant  
versions of a human interleukin-1 (IL-1) receptor antagonist protein.

CC The sequences encode mutants MILRA-3, MILRA-2 and MILRA-1  
CC respectively, which contain at least one of the following two  
CC substitutions: Asn to Arg at position 91 of the mature protein or  
CC Thr to Ala at position 109 of the mature protein. The IL-1 receptor  
CC antagonist mutants have an improved capacity for interaction with  
CC IL-1 receptor type I (largely responsible for cell activation in  
CC response to IL-1). The mutant proteins can be used in the prepn. of  
CC drugs capable of antagonising the inflammatory, neurological, and  
CC endocrinological, haematological, metabolic, catabolic and  
CC immunostimulant effects associated with IL-1, and in particular for  
CC the treatment of acute or chronic inflammatory pathologies e.g.  
CC rheumatoid arthritis. 135 A; 147 C; 132 G; 117 T;  
SQ Sequence 531 BP; 79.4%; Score 460; DB 22; Length 531;  
Best Local Similarity 99.1%; Pred. No. 1.40e-295;  
Matches 464; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
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QY 106 GAGACGATCTCCGACCTCTGGAGAAATCCAGCAAGATGCAAGCCTTCAGATCTGG 165  
Db 124 gatgttaaccagaagaccttctatctgaggaacaaccaactagttgtggtacttgcaa 183  
QY 166 GATGTTAAACAGAGACCTTCTATCTGAGGAACAACCAACTAGTTGCTGGATCTGCA 225  
Db 184 ggacaaatgcaatttagagaagaaatagatgtgtggtacccattgagcctcatgctctg 243  
QY 226 GGACCAATGCAATTTAGAGAAAGATAGATGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 285  
Db 244 ttcttggaatccatgaggggaagatgtgctgctgctgctgctgctgctgctgctgctg 303  
QY 286 TTCTTGGGAATCCATGAGGGAAGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 345  
Db 304 agactccagctgagggcagttacatcactgacgtgagcgagggcgagaaagcaggaag 363  
QY 346 AGACTCCAGCTGGAGGAGTTAATCATCTGACCTGAGCGAGAACAGAAAGCAGGACAAG 405  
Db 364 cgcttcgcttcacgtcagacagtgagtgagtgagtgagtgagtgagtgagtgagtgag 423  
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Db 424 ccggttggttctctcagcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 483  
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Db 484 cctgacgaagcgctcatggtggtcaccacaaattctacttccagggagagag 531  
QY 526 CTTGACGAAGGCGTCATGGTCAACCAATTTCTACTTCCAGGAGGAGGAGGAGGAGGAG 573

Search completed: Thu Feb 19 10:01:31 1998  
Job time : 104 secs.



(TM)

Database:

EST-B

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99:EST99 100:EST100 101:EST101 102:EST102 103:EST103

104:EST104 105:EST105 106:EST106 107:EST107 108:EST108

109:EST109 110:EST110 111:EST111 112:EST112 113:EST113

114:EST114 115:EST115 116:EST116 117:EST117 118:EST118

119:EST119 120:EST120 121:EST121 122:EST122 123:EST123

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174:EST174 175:EST175 176:EST176 177:EST177 178:EST178

## SUMMARIES

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1	342	59.1	435	158	W78043	zd72d01.r1 Soares fet	0.00e+00	
2	331	57.2	442	135	W95637	ze06f10.r1 Soares fet	0.00e+00	
3	243	42.0	260	27	R46971	y754f05.r1 Homo sapie	0.00e+00	
4	228	39.4	281	28	R50441	y758a03.r1 Homo sapie	0.00e+00	
5	217	37.5	401	24	R34906	y959e06.r1 Homo sapie	0.00e+00	
6	66	11.4	234	51	R83257	yP08h09.r1 Homo sapie	6.48e-74	
7	34	5.9	482	47	H50548	yP08h09.s1 Homo sapie	6.16e-20	
C	8	29	5.0	479	188	AA030324	mi08c10.r1 Soares mou	1.02e-12
C	9	25	4.3	114	1	HUM21ES27	Homo sapiens expresse	2.10e-07
C	10	25	4.3	202	193	AA143899	zEST00702 Maize leaf,	2.10e-07
C	11	25	4.3	229	17	T18787	zEST00203-5 Zea mays	2.10e-07
C	12	25	4.3	312	58	T28729	EST53526 Homo sapiens	2.10e-07
C	13	25	4.3	348	23	R31397	yH75g07.r1 Homo sapie	2.10e-07
C	14	25	4.3	407	1	R01304	yH77g06.r1 Homo sapie	2.10e-07
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17	24	4.1	308	183	H39468	SW3IC0487SK Onchocerc	3.72e-06	
C	18	24	4.1	326	177	AA190058	mu53b12.r1 Soares mou	3.72e-06
19	24	4.1	433	109	W53364	md42b07.r1 Soares mou	3.72e-06	
20	24	4.1	448	183	MTCC32	M.musculus mRNA; expr	3.72e-06	
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C	22	24	4.1	484	50	R30034	15639 Arabidopsis thal	3.72e-06
C	23	24	4.1	1024	127	W93377	mb99a06.r1 Soares mou	3.72e-06
24	23	4.0	346	185	R86352	SW3IC0515SK Onchocerc	6.05e-05	
C	25	23	4.0	362	57	T21091	3099 Arabidopsis thal	6.05e-05
C	26	23	4.0	401	62	T76094	10872 Arabidopsis thal	6.05e-05
C	27	23	4.0	443	66	H35048	EST109581 Rattus sp.	6.05e-05
C	28	23	4.0	464	170	AA152367	zo07b06.s1 Strategene	6.05e-05
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31	23	4.0	555	109	W52561	zc94g07.r1 Pancratic	6.05e-05	
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## ALIGNMENTS

[illegible]

SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 435)  
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
 TITLE The WashU-Merck EST Project  
 JOURNAL Unpublished (1995)  
 COMMENT Contact: Wilton RK  
 WashU-Merck EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.wustl.edu  
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
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 Location/Qualifiers  
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 /note="Organ: heart; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGGCGGCGCCGATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Boudado. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBHL19W."  
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 Matches 343; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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 QY 295 ATCCATGGGGAGAGATGTGCTCTCTCTGTCTCAAGTCGTGTGATGACACGACTCCAG 354  
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 QY 355 CTGGAGGCAGTAAATCATCTACCTGACCTGAGCGAGAACAGAGAGAGAGAGAGAGAG 414  
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QY 535 GCGGTCAATGGTACCAGAAATCTTACTTCCAGGAGGAGGAGTAGTAC 579  
 RESULT 2 W95637 442 bp mRNA EST 16-JUL-1996  
 LOCUS ze06f10.r1 Soares fetal heart NBHL19W Homo sapiens cDNA clone  
 DEFINITION 358219 5' similar to gb:X64532\_rnal INTERLEUKIN-1 RECEPTOR  
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 W95637  
 ACCESSION  
 NID g1425546  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 442)  
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
 TITLE The WashU-Merck EST Project  
 JOURNAL Unpublished (1995)  
 COMMENT Contact: Wilton RK  
 WashU-Merck EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.wustl.edu  
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
 Seq primer: mob.REGA+ET  
 High quality sequence stop: 314.  
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 /note="Organ: heart; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGAAGGCGGCGCCGATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Boudado. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBHL19W."  
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 /sex="unknown"  
 /dev\_stage="19 weeks"  
 /lab\_host="DH10B (ampicillin resistant)"  
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 Matches 362; Conservative 0; Mismatches 3; Indels 5; Gaps 5;  
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 Db 125 gattgtaccaggaagacacctctctatctgaggaacacacacactagttgctggaactgcaa 184  
 QY 166 GATGTATACCAAGACCTTCTATCTGAGGAACAAACCACTAGTTGCTGGATCTGCAA 225  
 Db 185 ggaccacaaatgtaattagaagaaagatagatgtgtgtacccattgagcctcatgctctg 244

319	QY	TCTGTGTC	CAAGTCTGGTGATGAGACGAGCAGCTCCAGCTGGAGCGAGTTAACTACTGCAC	378
67	Ddb	ctgagcgcagacagaaaagcaggacagaagcgcttcgcgtccatccgctcagacagcgggcccc	126	
379	QY	CTGAGCGACAGACAGAAGCAGGACGAGCGCTTCGCCCTTCATCCGCTCAGACAGATGGCCCC	438	
127	Ddb	accaccagtgttgagctgccnctgcccngtgggtttcctctgcacagcgatggaagct	186	
439	QY	ACCACCAGTTTTGAGTCTCCGCGCTGCCCGGTTGGTTCTCTGCACAGCGATGAAGCT	498	
187	Ddb	gaccacccgctcagcctccaataatgctgacgaagcgctcatggtcaccaaatcttac	246	
499	QY	GACCACGCCGTGAGCTCACCAATATGCCTGACGAAGGCGTCATGGTCACCAAATTCTAC	558	
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559	QY	TTCCAGG	565	
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LOCUS		YJ58a03.r1 Homo sapiens CDNA clone 152908 5'		similar to
DEFINITION		9D:X64532_rnal INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (HUMAN);.		
ACCESSION		R50241		
NID		g812143		
KEYWORDS		Homo sapiens		
SOURCE		human clone=152908 library=Soares breast 2NDBst vector-pt7T3D (Pharmacia) with a modified polylinker host=DHI0B (ampicillin resistant) primer=M13RP1 RdteI+Not I Rsite+Eco RI Adult female. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTCGAGCGAGCGCGCCCTTTTTTTTTTTTTTTT 3', double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 230. Library constructed by Bento Soares and M.Fatima Bonaldo.		
ORGANISM		Homo sapiens		
REFERENCE		Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcophrygi; Chonadata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 281)		
AUTHORS		Hillier,L., Clark,N., Dubucque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasaki,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.		
TITLE		The WashU-Merck EST Project		
JOURNAL		Unpublished (1995)		
COMMENT		Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu High quality sequence stops: 273 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LNL; contact the IMAGE Consortium ( <a href="mailto:info@image.llnl.gov">info@image.llnl.gov</a> ) for further information. Location/Qualifiers 1..281 /organism="Homo sapiens" /clone="152908"		
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Matches		259;	Conservative 0;	Mismatches 1; Indels 5; Gaps 5;

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 QY 320 CCGTGTCAAGTCTGGTATGAGACCACTCCAGCTGGAGCGAGTTAACTCATCTGACC 379  
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 Db 68 tgagcagagacagaaagcagacagcgttccttcacccgctcagacagcgcccca 127  
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 QY 380 TGAGCAGAACAGAACAGACAGAGCGCTTCGGCTTCATCCGCTCAGACAGTGGCCCCA 439  
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 (HUMAN);  
 ACCESSION R34906  
 NID 9791807  
 KEYWORDS EST.  
 SOURCE human clone-36844 library-Soares infant brain LNTB vector-lafmid BA  
 host-DH10B (ampicillin resistant) primer-M13RPI Rsite1-Not I  
 Rsite2-Hind III Whole brain from a 73 days post natal female. 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5',  
 AACTCGAAGATTCGCGCGCAGCAATTTTCTTTTCTTTT 3']; double-stranded  
 cDNA was ligated to Hind III adaptors (Pharmacia), digested with  
 Not I and directionally cloned into the Not I and Hind III sites of  
 the lafmid BA vector. Library went through one round of  
 normalization. Library constructed by Bento Soares and M.Fatima  
 Bonaldo.  
 ORGANISM Homo sapiens  
 Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;  
 Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 401)  
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
 Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and  
 Wilson,R.  
 TITLE The WashU-Merck EST Project  
 JOURNAL Unpublished (1995)  
 COMMENT GDB: G00-409-345  
 Contact: Wilson RK  
 WashU-Merck EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 High quality sequence stops: 309  
 Source: IMAGE Consortium, LLNL  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 FEATURES  
 source Location/Qualifiers  
 1..401  
 /organism="Homo sapiens"  
 /clone="36844"

BASE COUNT 108 a 93 c 105 g 94 t 1 others  
 ORIGIN  
 Query Match 37.5%; Score 217; DB 24; Length 401;  
 Best Local Similarity 97.7%; Pred. No. 0.00e+00;

Matches 253; Conservative 0; Mismatches 0; Indels 6; Gaps 6;  
 Db 68 gagacgatccgacccctctggagaaaaatccagcaagatgcaagccttcagaatctgg 127  
 |||||  
 QY 106 GAGACGATCTCCGACCTCTGGGAGAAAATCCAGCAAGATGCAAGCTTCAGAATCTGG 165  
 |||||  
 Db 128 gattttaaccagaagacact 187  
 |||||  
 QY 166 GATGTTAACCAAGAAGACCTTCTATCTGAGGAACAACCAACTAGTTGCTGGTACTTGCAA 225  
 |||||  
 Db 188 ggaccaaagtcaatttagaagaaaaatagatgtgtaccattgacccatgacccatgctg 247  
 |||||  
 QY 226 GGACCAATGTCATTTAGAGAAAAGATAGATGTGTGCTGCTGCTGCTGCTGCTGCTG 285  
 |||||  
 Db 248 ttctgggggaatccatggaggggaagatgtgctgtctctgtgttcagtctgggtgatg 307  
 |||||  
 QY 286 TTCCTGGG-ATTCATGG-AGGG-AAGATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTG 340  
 |||||  
 Db 308 aggaccagactccagctgg 326  
 |||||  
 QY 341 AG-ACCAGACTCCAGCTGG 358  
 |||||

RESULT 6  
 LOCUS R83257 234 bp mRNA EST 04-AUG-1995  
 DEFINITION YP08h09.r1 Homo sapiens cDNA clone 186881 5' similar to  
 gp:X64532\_rnal INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR  
 (HUMAN);  
 ACCESSION R83257  
 NID 928134  
 KEYWORDS EST.  
 SOURCE human clone-186881 library-Soares breast 3NBHst vector-p77T3D  
 (Pharmacia) with a modified polylinker host-DH10B (ampicillin  
 resistant) primer-M13Rev Rsite1-Not I Rsite2-Eco RI Adult human.  
 1st strand cDNA was primed with a Not I - oligo(dT) primer [5',  
 TTTTACCAATCGAAGTGGAGCGCGCCCTTTTCTTTTCTTTT 3'],  
 double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),  
 digested with Not I and cloned into the Not I and Eco RI sites of a  
 modified p77T3 vector (Pharmacia). Library went through one round  
 of normalization to a Cot = 20. Library constructed by Bento Soares  
 and M.Fatima Bonaldo.  
 ORGANISM Homo sapiens  
 Eucaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
 Sarcopterygii; Choonata; Tetrapoda; Amniota; Mammalia; Theria;  
 Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 234)  
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
 Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and  
 Wilson,R.  
 TITLE The WashU-Merck EST Project  
 JOURNAL Unpublished (1995)  
 COMMENT Contact: Wilson RK  
 WashU-Merck EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 High quality sequence stops: 66  
 Source: IMAGE Consortium, LLNL  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 FEATURES  
 source Location/Qualifiers  
 1..234  
 /organism="Homo sapiens"  
 /clone="186881"

BASE COUNT 51 a 75 c 57 g 47 t 4 others  
 ORIGIN

Query Match 11.4%; Score 66; DB 51; Length 234;  
 Best Local Similarity 94.4%; Pred. No. 6.48e-74;  
 Matches 102; Conservative 0; Mismatches 0; Indels 6; Gaps 6;

Db 9 cctgtgtcagtcgtgtgagaccagagctccagctgagggcaggttaacatcact 68  
 QY 320 CCGTGTCAAGTCTGGTGATGAG-ACCAG-ACT-CCAGCTGGAGG-CAGTTAACATCACT 375  
 Dh 69 gaacctgagcggagacagagaagacagacagcgttcgccttcaccc 116  
 QY 376 GACGACAGAGACAGACAGACAGCGCTTCGCGCTTCATCC 421

RESULT 7  
 LOCUS H50548 482 bp mRNA EST 18-SEP-1995  
 DEFINITION yp08h09.s1 Homo sapiens cDNA clone 186881 3' similar to  
 gb:X64532\_rnal INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR  
 (HUMAN);  
 ACCESSION H50548  
 NID 9990389  
 KEYWORDS EST.  
 SOURCE human clone-186881 primer-Promega -2ml13 library-Soares breast  
 3nBHST vector-pT7T3D (Pharmacia) with a modified polylinker  
 host-DH10B (ampicillin resistant) Rsite1-Not I Rsite2-Eco RI Adult  
 human 1st strand cDNA was primed with a Not I - oligo(dT) primer  
 [5'] TGTTACCAATCTGAAGTGGAGCGCGCCGCTTTTCTTTTCTTTTCTTTT 3'],  
 double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),  
 digested with Not I and cloned into the Not I and Eco RI sites of a  
 modified pT7T3 vector (Pharmacia). Library went through one round  
 of normalization to a Cot = 20. Library constructed by Bento Soares  
 and M.Fatima Bonaldo.

ORGANISM Homo sapiens  
 Eukaryotes; Metazoa; Eumetazoa; Bilateria; Coelomata;  
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
 Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
 Eutheria; Archonta; Primates; Catarrhini; Hominiidae; Homo.  
 1 (bases 1 to 482)  
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
 Trevisakis,E., Waterston,R., Williamson,A., Wohlmann,P. and  
 Wilson,R.  
 TITLE The WashU-Merck EST Project  
 JOURNAL Unpublished (1995)  
 COMMENT Contact: Wilson RK  
 WashU-Merck EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 High quality sequence stops: 327  
 Source: IMAGE Consortium, LLNL  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES  
 source  
 1..482  
 /organism="Homo sapiens"  
 /clone="186881"  
 <1..>482

BASE COUNT 101 a 104 c 167 g 103 t 7 others

ORIGIN  
 Query Match 5.9%; Score 34; DB 47; Length 482;  
 Best Local Similarity 92.1%; Pred. No. 6.16e-20;  
 Matches 58; Conservative 0; Mismatches 1; Indels 4; Gaps 4;

Db 385 gtactactgcctcctcggagtagaattngt-accat-acgc-ttcgt-aggcatatt 440  
 Cp 579 GTACTACTGCTCTCTCTCGGAAGTAGAATTGGTGACCATGACGCTTCGTCGACGCATATT 520  
 Db 441 ggt 443

Cp 519 GGT 517

RESULT 8  
 LOCUS AA030324 479 bp mRNA EST 21-JAN-1997  
 DEFINITION mi08c10.r1 Soares mouse placenta 4NDMP13.5 14.5 Mus musculus cDNA  
 clone 459858 5'.  
 ACCESSION AA030324  
 NID 91497479  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Mus.  
 1 (bases 1 to 479)  
 AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
 Waterston,R.  
 TITLE The WashU-HIMI Mouse EST Project  
 JOURNAL Unpublished (1996)  
 COMMENT Contact: Marra M/Mouse EST Project  
 WashU-HIMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:276746  
 Seq primer: -28M13 rev2 from Amersham  
 High quality sequence stop: 467.

FEATURES  
 source  
 1..479  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /note="vector: pT7T3D-Pac (Pharmacia) with a modified  
 polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
 was primed with a Not I - oligo(dT) primer [5'  
 TGTTACCAATCTGAAGTGGAGCGCGCGCAATTTTTTTTTTTTTTTTTTTT  
 T 3']; double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified pT7T3 vector. Library  
 went through one round of normalization, and was  
 constructed by Bento Soares and M.Fatima Bonaldo."  
 /clone="459858"  
 /clone\_lib="Soares mouse placenta 4NDMP13.5 14.5"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 <1..>479

BASE COUNT 148 a 108 c 102 g 121 t

ORIGIN  
 Query Match 5.0%; Score 29; DB 188; Length 479;  
 Best Local Similarity 78.4%; Pred. No. 1.02e-12;  
 Matches 40; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Db 273 agtggtacaacctctacatttgatctgcagccttcctcgttggttcac 323  
 QY 430 AGTGGCCCCACCCACAGTTTGTGAGTCTGCCGCTGCCCGGTTGCTTCCTC 480

RESULT 9  
 LOCUS HW21ES27 114 bp mRNA EST 20-SEP-1994  
 DEFINITION Homo sapiens expressed sequence tag 21ES0027.  
 ACCESSION L25173  
 NID g540376

**Best Available Copy**

Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, P., Ferrlie, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Weissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.  
Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence  
Unpublished (1995)

Contact: Venter, JC  
The Institute for Genomic Research  
932 Clopper Rd, Gaithersburg, MD 20878  
Tel: 3018699056  
Fax: 3018699423

Email: tdbinfo@tdb.tigr.org

For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org).

Location/Qualifiers  
1..312  
/organism="Homo sapiens"

BASE COUNT 102 a 40 c 99 g 68 t 3 others  
ORIGIN

Query Match 4.3%; Score 25; DB 58; Length 312;  
Best Local Similarity 83.8%; Pred. No. 2.10e-07;  
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 60 tgaagaaggaggaggaagcagagagaggagagac 96  
|||||

QY 54 TGAAGAAGGAGGTGGAGGAGGAGGAGGAGGTGAAGAC 90  
|||||

RESULT 13  
LOCUS R31397 348 bp mRNA EST 28-APR-1995  
DEFINITION Yh75q07.r1 Homo sapiens cDNA clone 135612 5'.  
ACCESSION R31397  
NID 9787240  
KEYWORDS EST.  
SOURCE human clones-135612 library-Soares placenta Nb2HP vector-pTT73D (Pharmacia) with a modified polylinker host-DH10B (ampicillin resistant) primer-M13RP1 Rsite1-Not I Rsite2-Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer [5',

AACTGGAGAAATTCGGCCGAGGAATTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens  
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 348)  
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 259

Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
FEATURES  
source  
1..348  
/organism="Homo sapiens"  
/clone="135612"

BASE COUNT 118 a 43 c 107 g 79 t 1 others  
ORIGIN

Query Match 4.3%; Score 25; DB 23; Length 348;  
Best Local Similarity 83.8%; Pred. No. 2.10e-07;  
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 58 tgaagaaggaggaggaagcagagagaggagagac 94  
|||||

QY 54 TGAAGAAGGAGGTGGAGGAGGAGGAGGAGGTGAAGAC 90  
|||||

RESULT 14  
LOCUS R01304 407 bp mRNA EST 31-MAR-1995  
DEFINITION ye77d06.r1 Homo sapiens cDNA clone 123755 5'.  
ACCESSION R01304  
NID 9751040  
KEYWORDS EST.  
SOURCE human clones-123755 library-Soares fetal liver spleen lNPLS vector-pTT73D (Pharmacia) with a modified polylinker host-DH10B (ampicillin resistant) primer-M13RP1 Rsite1-Pac I Rsite2-Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5',

AACTGGAGAAATTAATGAACATTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pTT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens  
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 407)  
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 264

Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES  
source  
1..407  
/organism="Homo sapiens"  
/clone="123755"

BASE COUNT 115 a 70 c 117 g 101 t 4 others  
ORIGIN

Query Match 4.3%; Score 25; DB 1; Length 407;  
Best Local Similarity 83.8%; Pred. No. 2.10e-07;  
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 226 tgaagaaggaggaggaagcagagagaggagagac 262  
|||||

QY 54 TGAAGAAGGAGGTGGAGGAGGAGGAGGAGGTGAAGAC 90  
|||||

High quality sequence stops: 259

```

RESULT 15
LOCUS      434 bp      mRNA      20-AUG-1996
DEFINITION      zB45a07.r1 Soares fetal lung NBHL19W Homo sapiens CDNA clone 306516
                    5',
ACCESSION      W31239
NID            91312231
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
               Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
               Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 434)
AUTHORS        Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
               Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
               Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevasakis,E.,
               Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
               WashU-Merck EST Project
               Unpublished (1995)

TITLE          zB45a07.r1 Soares fetal lung NBHL19W Homo sapiens CDNA clone 306516
JOURNAL
ENTRY

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 878 Std Error: 0.00
Seq primer: mob.REGA-EF
High quality sequence stop: 345.
Location/Qualifiers
1..434
/organism="Homo sapiens"
/notes="Organ: lung; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
15'-GTGTACCAATCTGAGTGGAGCGCGCAATTTTTTTTTTTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaïdo. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NBHL19W."
/clone="306516"
/clone.lib="Soares fetal lung NBHL19W"
/dev_stage="19 weeks"
/lab_host="DB10B (ampicillin resistant)"
<1..>434

BASE COUNT      136 a      68 c      126 g      104 t

Query Match      4.3%; Score 25; DB 128; Length 434;
Best Local Similarity 83.8%; Pred. No. 2.10e-07;
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Ddb 179 tgaagaagaggaggaagaggcagcagaagaggagac 215
|||||
|||||
|||||
|||||
|||||

OY 54 TCAGAGAGGAGGTGGAGGAGGAGGAGAGAGGTGAGAC 90
|||||
|||||
|||||
|||||
|||||

Search completed: 1998-FEB-19 10:11:32 1998
Job time : 569 secs.

```



\*\*\*\*\*  
MPSchpp protein - protein database search, using Smith-Waterman algorithm  
\*\*\*\*\*  
(TM)  
\*\*\*\*\*

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Run on: Thu Feb 19 10:10:06 1998; MasPar time 8.19 Seconds  
669.652 Million cell updates/sec  
ar output not generated.  
Title: >US-08-910-733-13  
Description: (1-180) from US08910733.pep  
Perfect Score: 1298  
Sequence: 1 MALADLYEEGGGGGEGEDN.....LTNMPDEGMVMTKFFQDE 180

Scoring table: PAM 150  
Gap 11  
Searched: 95051 seqs, 30469580 residues  
Post-processing: Minimum Match 0%  
Listing first 45 summaries  
Database: p1r53  
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3  
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8  
13:unann9 14:unann10 15:unann11 16:unann12 17:unann  
18:unrev

Statistics: Mean 42.369; Variance 82.094; scale 0.516  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES				
Rd	No.	Score	Match Length DB ID	Description
1	1298	100.0	180 6 A39386	interleukin-1 recept 3.11e-247
2	1140	87.8	177 6 A30368	interleukin-1 recept 5.41e-213
3	965	74.3	177 6 A54377	interleukin-1 recept 2.82e-175
4	955	73.6	178 6 A44610	interleukin-1 recept 3.96e-173
5	905	69.7	178 6 C40956	interleukin-1 recept 2.08e-162
6	251	19.3	68 6 B54377	interleukin-1 recept 2.20e-27
7	230	17.7	269 2 I55969	interleukin-1 beta p 1.84e-23
8	229	17.6	266 2 ICB01B	interleukin-1 beta p 2.82e-23
9	228	17.6	266 2 S23010	interleukin-1 beta p 4.31e-23
10	214	16.5	267 6 S38373	interleukin-1 beta p 1.60e-20
11	205	15.8	267 2 JN0724	interleukin-1 beta p 6.87e-19
12	200	15.4	269 2 ICH01B	interleukin-1 beta p 5.45e-18
13	195	15.0	268 2 A30584	interleukin-1 beta p 4.27e-17
14	96	7.4	370 12 I40358	N-acyl-L-amino acid 3.36e-01
15	93	7.2	432 16 A34448	thrombin receptor - 8.33e-01
16	92	7.1	1024 12 C64208	hypothetical protein 1.12e+00
17	91	7.0	490 6 S31450	1-aminocyclopropane- 1.51e+00
18	89	6.9	219 14 S66947	hypothetical protein 2.70e+00
19	89	6.9	396 4 A54536	translation elongati 2.70e+00
20	89	6.9	795 8 I50255	108K heat shock prot 2.70e+00

21	89	6.9	795 3 HHCH08	heat shock protein 1	2.70e+00
22	88	6.8	157 13 S49793	hypothetical protein	3.61e+00
23	88	6.8	442 1 B43362	protein-tyrosine kin	3.61e+00
24	88	6.8	841 5 S34624	glycogen phosphoryla	3.61e+00
25	88	6.8	842 5 A27335	glycogen phosphoryla	3.61e+00
26	88	6.8	843 1 PHRBG	glycogen phosphoryla	3.61e+00
27	88	6.8	974 5 A49714	protein-tyrosine kin	3.61e+00
28	88	6.8	2317 5 I56752	c-ras-1 tyrosine kin	3.61e+00
29	88	6.8	2338 5 I73957	c-ras-1 tyrosine kin	3.61e+00
30	87	6.7	307 12 G64239	Holliday junction DN	4.81e+00
31	87	6.7	496 6 A47199	1-aminocyclopropane-	4.81e+00
32	87	6.7	496 6 S46189	1-aminocyclopropane-	4.81e+00
33	86	6.6	488 6 JC4549	1-aminocyclopropane-	6.38e+00
34	86	6.6	847 5 A35518	glycogen phosphoryla	6.38e+00
35	84	6.5	244 6 A35227	H+-transporting ATP	1.12e+01
36	84	6.5	362 7 S50993	ribosomal protein L4	1.12e+01
37	84	6.5	362 7 S45887	ribosomal protein L4	1.12e+01
38	85	6.5	387 10 S52274	Nusa protein - Therm	8.46e+00
39	85	6.5	481 12 S69808	lincomycin resistanc	8.46e+00
40	84	6.5	803 8 A35954	endoplasmic precurs	1.12e+01
41	84	6.5	804 8 S51358	protein kinase ppk98	1.12e+01
42	84	6.5	804 8 A53211	glucose-regulated pr	1.12e+01
43	84	6.5	1522 14 S48904	probable purine nucl	1.12e+01
44	83	6.4	336 14 S52691	probable membrane pr	1.47e+01
45	83	6.4	1411 14 S55123	hypothetical protein	1.47e+01

ALIGNMENTS

RESULT	1	A39386	#type complete
ENTRY		interleukin-1 receptor antagonist, long intracellular splice	
TITLE		form - human	
CONTAINS		interleukin-1 receptor antagonist, short intracellular splice	
ORGANISM		#formal_name Homo sapiens #common_name man	
DATE		28-Feb-1992 #sequence_revision 11-Apr-1997 #text_change	
ACCESSIONS		I37893; A39386	
REFERENCE		I37893	
#authors		Muzio, M.; Polentarutti, N.; Sironi, M.; Poli, G.; De Gioia, L.; Introna, M.; Mantovani, A.; Colotta, F.	
#journal		J. Exp. Med. (1995) 182:623-628	
#title		Cloning and characterization of a new isoform of the interleukin 1 receptor antagonist.	
#cross-references		MUID:95355865	
#accession		I37893	
#status		translated from GB/EMBL/DBJ	
#molecule_type		mRNA	
#residues		1-180 #label RES	
#cross-references		EMBL:X84348; NID:g1008970; CDS_PID:g1008971	
REFERENCE		A39386	
#authors		Haskill, S.; Martin, G.; Van Le, L.; Morris, J.; Peace, A.; Bigler, C.F.; Jaffe, G.J.; Hammerberg, C.; Sporn, S.A.; Fong, S.; Arend, W.P.; Ralph, P.	
#journal		Proc. Natl. Acad. Sci. U.S.A. (1991) 88:3681-3685	
#title		CDNA cloning of an intracellular form of the human interleukin 1 receptor antagonist associated with epithelium.	
#cross-references		MUID:91219436	
#accession		A39386	
#molecule_type		mRNA	
#residues		1-3,25-180 #label HAS	
#cross-references		GB:M55646	
GENETICS			
#gene		GDB:IL1RN	
#cross-references		GDB:125897	
#map position		2q14.2-2q14.2	
CLASSIFICATION		#superfamily interleukin-1	
KEYWORDS		alternative splicing; cytokine receptor	
FEATURE		#product interleukin-1 receptor antagonist, long intracellular splice form #status predicted #label	
1-180			

```

1-3,25-180      MAIN
#product interleukin-1 receptor antagonist, short
#intracellular splice form #status predicted #label MA2
SUMMARY          #length 180 #molecular-weight 19897 #checksum 956

Query Match      100.0%; Score 1298; DB 6; Length 180;
Best Local Similarity 100.0%; Pred. No. 3.11e-247;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 maladiyegggggednadsketicrpsgrksskmqafriwdvngktylrnnqlva 60
QY 1 MALADLYEEGGGGEGEDNADSKETICRPSGRKSSKMQAFRIWDVNGKTYLRNNQLVA 60

Db 61 gylggnvnleekidvvpiephalfihggkmlscvksdetrqlgleavnitdlsenr 120
QY 61 GYLGQPNVNLKEEKIDVVPIEPHALFLIHGGKMLSCVKSDETRQLGLEAVNITDLSNR 120

Db 121 kqdkrfafirsdsgpttsfesaacpgwflctameadqpsvltmnpdegvmvtkfyfgede 180
QY 121 KQDKRFARIRSDSGPTTSFESAACPGWFLCTAMEADQPSVLTNMPDEGMVMTKIFYQEDE 180

RESULT 2          A30368 #type complete
ENTRY      interleukin-1 receptor antagonist secreted form precursor -
TITLE      human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change
23-May-1997
ACCESSIONS  A40956; I37894; A30368; S08160; S08159; A37822
REFERENCE    #authors Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.;
Brandhuber, B.J.; Thompson, R.C.
#journal     Proc. Natl. Acad. Sci. U.S.A. (1991) 88:5232-5236
#title       Interleukin 1 receptor antagonist is a member of the
interleukin 1 gene family: evolution of a cytokine control
mechanism.
#cross-references MUID:91271363
#accession   A40956
#molecule_type DNA
#residues    1-177 #label EIS
#cross-references GB:M63099
REFERENCE    I37894
#authors     Lennard, A.; Gorman, P.; Carrier, M.; Griffiths, S.; Scotney,
H.; Sheer, D.; Solari, R.
#journal     Cytokine (1992) 4:83-89
#title       Cloning and chromosome mapping of the human interleukin-1
receptor antagonist gene.
#cross-references MUID:92338323
#accession   I37894
#molecule_type DNA
#status      translated from GB/EMBL/DBJ
#residues    1-177 #label LEN
#cross-references EMBL:X64532; NID:g33798; CDS_PID:g33799
REFERENCE    A30368
#authors     Carter, D.B.; Delbel Jr., M.R.; Dunn, C.J.; Tomich, C.S.C.;
Laborde, A.L.; Slightom, J.L.; Berger, A.E.; Bienkowski,
M.J.; Sun, F.F.; McEwan, R.N.; Harris, P.K.W.; Yem, A.W.;
Waszak, G.A.; Chosay, J.G.; Siew, L.C.; Hardee, M.M.;
Zurcher-Neely, H.A.; Reardon, I.M.; Heinrichson, R.L.;
Truesdell, S.E.; Shelly, J.A.; Bessalu, T.E.; Taylor, B.M.;
Tracey, D.E.
#journal     Nature (1990) 344:633-638
#title       Purification, cloning, expression and biological
characterization of an interleukin-1 receptor antagonist
protein.
#cross-references MUID:90220867
#accession   A30368
#molecule_type mRNA
#residues    1-177 #label CAR
#cross-references GB:X53296
#note        parts of this sequence, including the amino end of the
mature protein, were confirmed by peptide sequencing

```

```

REFERENCE S08160
#authors   Eisenberg, S.P.; Evans, R.J.; Arend, W.P.; Verderber, E.;
Brewer, M.T.; Hannum, C.H.; Thompson, R.C.
#journal   Nature (1990) 343:341-346
#title     Primary structure and functional expression from
complementary DNA of a human interleukin-1 receptor
antagonist.
#cross-references MUID:90136921
#accession S08160
#status    not compared with conceptual translation
#molecule_type mRNA
#residues  1-177 #label E12
REFERENCE S08159
#authors   Hannum, C.H.; Wilcox, C.J.; Arend, W.P.; Joslin, F.G.;
Dripps, D.J.; Heimdal, P.L.; Armes, L.G.; Sommer, A.;
Eisenberg, S.P.; Thompson, R.C.
#journal   Nature (1990) 343:336-340
#title     Interleukin-1 receptor antagonist activity of a human
interleukin-1 inhibitor.
#cross-references MUID:90136920
#accession S08159
#molecule_type protein
#residues  26-75;97-108;110-116;120-131;163-176 #label HAN
REFERENCE A37822
#authors   Bienkowski, M.J.; Bessalu, T.E.; Berger, A.E.; Truesdell,
S.E.; Shelly, J.A.; Laborde, A.L.; Zurcher-Neely, H.A.;
Reardon, I.M.; Heinrichson, R.L.; Chosay, J.G.; Tracey, D.E.
#journal   J. Biol. Chem. (1990) 265:14505-14511
#title     Purification and characterization of interleukin 1 receptor
level antagonist proteins from THP-1 cells.
#cross-references MUID:90354444
#accession A37822
#molecule_type protein
#residues  26-52;70-77;122-127;170-175 #label BIE
#experimental_source culture medium, PMA-stimulated THP-1 cells
GENETICS
#gene       GDB:ILIRN
#cross-references GDB:125897
#map_position 2q14.2-2q14.2
#introns    39/2; 69/1; 106/3
CLASSIFICATION
#superfamily interleukin-1
KEYWORDS     alternative splicing; cytokine receptor; extracellular
protein; glycoprotein
FEATURE
1-25         #domain signal sequence #status experimental #label SIG
26-177       #product interleukin-1 receptor antagonist #status
experimental #label MAP
109          #binding_site carbohydrate (Asn) (covalent) #status
experimental
SUMMARY      #length 177 #molecular-weight 20055 #checksum 193
Query Match  87.8%; Score 1140; DB 6; Length 177;
Best Local Similarity 100.0%; Pred. No. 5.41e-213;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 22 eticrpsgrksskmqafriwdvngktylrnnqlvaglyggnvnleekidvvpiephal 81
QY 25 ETICRPSGRKSSKMQAFRIWDVNGKTYLRNNQLVAGLYGQPNVNLKEEKIDVVPIEPHAL 84
Db 82 flghggkmlscvksdetrqlgleavnitdlsenrkdkrfafirsdsgpttsfesaac 141
QY 85 FLGIHGGKMLSCVKSDETRQLGLEAVNITDLSNRKDKRFARIRSDSGPTTSFESAAC 144
Db 142 pgwflctameadqpsvltmnpdegvmvtkfyfgede 177
QY 145 PGWFLCTAMEADQPSVLTNMPDEGMVMTKIFYQEDE 180

RESULT 3
ENTRY      A54377 #type complete
TITLE      interleukin-1 receptor antagonist secreted form precursor -
rabbit
ORGANISM    #formal_name Oryctolagus cuniculus #common_name domestic

```

```

rabbit
06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change
23-May-1997
A54377; I46729
REFERENCE
#accessions A54377
#authors Cominelli, F.; Bortolami, M.; Pizarro, T.T.; Monsacchi, L.;
Ferrelli, M.; Brewer, M.T.; Eisenberg, S.P.; Ng, R.K.
#journal J. Biol. Chem. (1994) 269:6962-6971
#title Rabbit interleukin-1 receptor antagonist. Cloning,
expression, functional characterization, and regulation
during intestinal inflammation.
#cross-references MUID:94165101
#accession A54377
##molecule_type mRNA
##residues 1-177 #label COM
##cross-references NCBI:144168; NCBI:144169
##experimental_source colon tissue
##note I46729 sequence extracted from NCBI backbone
REFERENCE
#accessions I46729
#authors Goto, F.; Goto, K.; Miyata, T.; Ohkawara, S.; Takao, T.;
Mori, S.; Furukawa, S.; Maeda, T.; Iwanaga, S.; Shimonishi,
Y.; Yoshinaga, M.
#journal Immunology (1992) 77:235-244
#title Interleukin-1 receptor antagonist in inflammatory exudate
cells of rabbits. Production, purification and
determination of primary structure.
#cross-references MUID:93052512
#accession I46729
##status translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-177 #label GOT
##cross-references GB:D21832; NID:g425787; CDS_PID:g452205
CLASSIFICATION #superfamily interleukin-1
KEYWORDS cytokine receptor; extracellular protein; glycoprotein
FEATURE
1-25 #domain signal sequence #status predicted #label SIG\
109 #binding_site carbohydrate (Asn) (covalent) #status
125 predicted
SUMMARY
#length 177 #molecular-weight 20214 #checksum 847
Query Match 74.3%; Score 955; DB 6; Length 177;
Best Local Similarity 78.2%; Pred. No. 2,82e-175;
Matches 122; Conservative 24; Mismatches 10; Indels 0; Gaps 0;
Db 22 etacpgrkprcmqafriwdvngkfylnnqlvagylggnakleeridvvpqll 81
QY 25 ETICRPSGRKSKMqAFRIWDVNGKTFYLRNQLVAGYLGQPNVLEEKIDVVPIDPHAL 84
Db 82 fligrgklclscvsgdkmklhlaevnldlgkneqdkfrfirsngpttffesasc 141
QY 85 FLGIHGRKMLCSVKSGDTRQLQLEAVNITDLSENKQDKRFAFIRSDSGPTTSFESAC 144
Db 142 pwwfictaleadqpsltnpddsiwvtfkyfqedq 177
QY 145 PGWFLCTAMEADQPSVLTNMPDEGVMTREYFQEDE 180

RESULT 4
ENTRY #type complete
TITLE interleukin-1 receptor antagonist precursor - mouse
ALTERNATE_NAMES IL-1ra
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change
23-May-1997
A44610; B40956; A49031; I56106; I52970
REFERENCE A44610
#authors Matsushima, H.; Roussel, M.F.; Matsushima, K.; Hishinuma, A.;
Sherr, C.J.
#journal Blood (1991) 78:616-623
#title Cloning and expression of murine interleukin-1 receptor
antagonist in macrophages stimulated by colony-stimulating
factor 1.
#accession A44610

```

```

##molecule_type mRNA
##residues 1-178 #label MAT
##cross-references GB:M64404
REFERENCE A40956
#authors Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.;
Brandhuber, B.J.; Thompson, R.C.
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:5232-5236
#title Interleukin 1 receptor antagonist is a member of the
interleukin 1 gene family: evolution of a cytokine control
mechanism.
#cross-references MUID:91271363
#accession B40956
##molecule_type DNA
##residues 7-178 #label EIS
##cross-references GB:M63100
REFERENCE A49031
#authors Shuck, M.E.; Eessalu, T.E.; Tracey, D.E.; Bienkowski, M.J.
#journal Eur. J. Immunol. (1991) 21:2775-2780
#title Cloning, heterologous expression and characterization of
murine interleukin 1 receptor antagonist protein.
#cross-references MUID:92037824
#accession A49031
##molecule_type mRNA
##residues 23-178 #label SHU
##cross-references NCBI:64082; NCBI:64085
##experimental_source peritoneal macrophages, ICR strain
##note I56106 sequence extracted from NCBI backbone
REFERENCE I56106
#authors Zahedi, K.; Seldin, M.F.; Rits, M.; Ezekowitz, R.B.;
Whitehead, A.S.
#journal J. Immunol. (1991) 146:4228-4233
#title Mouse IL-1 receptor antagonist protein: Molecular
characterization, gene mapping, and expression of mRNA in
vitro and in vivo.
#cross-references MUID:91250712
#accession I56106
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-178 #label RES
##cross-references GB:M74294; NID:g198387; CDS_PID:g198388
REFERENCE I52970
#authors Zahedi, K.A.; Uhlar, C.M.; Rits, M.; Prada, A.E.; Whitehead,
A.S.
#journal Cytokine (1994) 6:1-9
#title The mouse interleukin 1 receptor antagonist protein: gene
structure and regulation in vitro.
#cross-references MUID:94271931
#accession I52970
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type DNA
##residues 1-178 #label RE2
##cross-references GB:L32838; NID:g487864; CDS_PID:g528978
GENETICS
#gene IL-1rn
#introns 40/2; 70/1; 107/3
CLASSIFICATION #superfamily interleukin-1
KEYWORDS cytokine receptor
FEATURE
1-26
27-178
#domain signal sequence #status predicted #label SIG\
#product interleukin-1 receptor antagonist #status
predicted #label MA2
SUMMARY
#length 178 #molecular-weight 20274 #checksum 8941
Query Match 73.6%; Score 955; DB 6; Length 178;
Best Local Similarity 76.3%; Pred. No. 3.96e-173;
Matches 119; Conservative 25; Mismatches 12; Indels 0; Gaps 0;
Db 23 eaacpgrkprcmqafriwdvngkfylnnqlvagylggnakleeridvvpqllhsv 82
QY 25 ETICRPSGRKSKMqAFRIWDVNGKTFYLRNQLVAGYLGQPNVLEEKIDVVPIDPHAL 84
Db 83 fligrgklclscvsgdkmklhlaevnldlgkneqdkfrfirsngpttffesasc 142

```

KEYWORDS	cytokine receptor
SUMMARY	#length 68 #checksum 2056
Query Match	19.3%; Score 251; DB 6; Length 68;
Best Local Similarity	79.5%; Pred. No. 2,20e-27;
Matches	31; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
Ddb	30 asetaacrpqkrcrmqafriwdvqkfyfyrlnnqlvag 68
QY	23 SKETICRPSGRKSKMQAFRIWDVQKFYFRLNNQLVAG 61
RESULT 7	
ENTRY	155969 #type complete
TITLE	interleukin-1 beta precursor - mouse
ALTERNATE_NAMES	hematopoietin-1; IL-1 beta
ORGANISM	#formal_name Mus musculus #common_name house mouse
DATE	26-Jul-1996 #sequence_revision 22-Nov-1996 #text_change 16-Feb-1997
ACCESSIONS	155969; A24719; S13029
REFERENCE	155969
authors	Gray, P.W.; Glaister, D.; Chen, E.; Goeddel, D.V.; Pennica, D.
#journal	J. Immunol. (1986) 137:3644-3648
#title	Two interleukin 1 genes in the mouse: Cloning and expression of the cDNA for murine interleukin 1-beta.
#cross-references	MUID:87058957
#accession	155969
#status	preliminary; translated from GB/EMBL/DDBJ
#molecule_type	mRNA
#residues	1-269 #label RES
#cross-references	GB:M15131; NID:gi98293; CDS_PID:g309398
REFERENCE	A24719
authors	Telford, J.L.; Macchia, G.; Massone, A.; Carinci, V.; Palla, E.; Melli, M.
#journal	Nucleic Acids Res. (1986) 14:9955-9963
#title	The murine interleukin 1-beta gene: structure and evolution.
#cross-references	MUID:87117546
#accession	A24719
#molecule_type	mRNA
#residues	1-269 #label TEL
REFERENCE	S13029
authors	Daumy, G.O.; Wilder, C.L.; Merenda, J.M.; McColl, A.S.; Geoghegan, K.F.; Otterness, I.G.
#journal	FEBS Lett. (1991) 278:98-102
#title	Reduction of biological activity of murine recombinant interleukin-1beta by selective deamidation at asparagine-149.
#cross-references	MUID:91130610
#accession	S13029
#status	preliminary
#molecule_type	protein
#residues	118-269 #label DAU
COMMENT	This protein lacks a conventional signal sequence for protein export. Cleavage of a long N-terminal propeptide occurs with secretion, although uncleaved forms are also released. The uncleaved form of interleukin-beta, unlike interleukin 1-alpha, is inactive.
COMMENT	Interleukin-beta precursor is less heavily myristoylated than interleukin-1alpha precursor.
GENETICS	
#gene	IL-1-beta
CLASSIFICATION	#superfamily interleukin-1
KEYWORDS	cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
FEATURE	#product interleukin-1 beta #status experimental #label 111
SUMMARY	#length 269 #molecular-weight 30931 #checksum 8753
Query Match	17.7%; Score 230; DB 2; Length 269;
Best Local Similarity	30.7%; Pred. No. 1.84e-23;
Matches	42; Conservative 34; Mismatches 53; Indels 8; Gaps 7;

Query Match	17.6%	Score 229;	DB 2;	Length 266;
Best Local Similarity	37.1%	Pred. No. 2,82e-23;		
Matches	33;	Conservative 17;	Mismatches 37;	Indels 2; Gaps 2;
Ddb	173	lgikdnlylscvkkgdptqlgleavd-pkypvkrnmekrfvykteikntvefesvlyp	231	
QOY	86	LGIHGGKMLSCVKSQDETQLGLEAVNTDLSENRRQDKRFAFINRSDSGPTTFESAACP	145	
Ddb	232	nwyistsgleerpfvlghfrg-qgqditdf	259	
QOY	146	GWFLCTAMEADQPVSLTNMPDEGVAVTKF	174	
RESULT ENTRY	9	S23010	#type complete	

```

REFERENCE
  A61246
  Andrews, A.E.; Barcham, G.J.; Brandon, M.R.; Nash, A.D.
  Immunology (1991) 74:453-460
  #authors
  #journal
  #title
  Molecular cloning and characterization of ovine IL-1alpha and
  IL-1beta.
  #accession
  B61246
  #molecule_type
  mRNA
  #residues
  1-144, 'L', 146-266
  #label
  AND
  COMMENT
  This protein lacks a conventional signal sequence for protein
  export. Cleavage of a long N-terminal propeptide occurs with
  secretion, although uncleaved forms are also released. The
  uncleaved form of interleukin-1beta, unlike interleukin 1-alpha,
  is inactive.
  #comment
  Interleukin-1beta precursor is less heavily myristoylated than
  interleukin-1alpha precursor.
  CLASSIFICATION
  #superfamily
  interleukin-1
  KEYWORDS
  cytokine; immunoregulation; inflammation; lymphokine;
  macrophage; mitogen
  FEATURE
  114-266
  #product
  interleukin-1 beta
  #status
  predicted
  #label
  MAT
  SUMMARY
  #length
  266
  #molecular_weight
  30717
  #checksum
  1102

```

```

Query Match      17.6%; Score 228; DB 2; Length 266;
Best Local Similarity 37.1%; Pred. No. 4,31e-23;
Matches 33; Conservative 16; Mismatches 38; Indels 2; Gaps 2;

Ddb 173 lqirdknllyscvkgdttltgleevd-pkvyppkrnmekrfvfyktekntvfesvlyp 231
      ||| : : |||| | |||| : : : ||| : : ||| |
QY 86 LGIHGKMKLSCVSGDETRLQLEAVNITLSENRRKQDKRFARISDSGPTTFSFAACP 145

Ddb 232 nwyistsqieekpvlgrfrg-gqditdf 259
      || : : ||| |
QY 146 GWFLCTAMEADQPVSILTNMPDEGVVMTKF 174

```

RESULT	9	
ENTRY	S23010	#type complete

```

RESULT 10          S38373      #type complete
ENTRY             interleukin-1 beta precursor - pig
TITLE             #formal_name Sus scrofa domestica #common_name domestic pig
ORGANISM          20-May-1994 #sequence_revision 01-Dec-1995 #text_change
DATE              03-May-1996

ACCESSIONS        S38373
REFERENCE          S38373
#authors          Vandenbroeck, K.; Fiten, P.; Beuken, E.; Martens, E.;
#journal          Janssen, A.; van Damme, J.; Opdenakker, G.; Billiau, A.
#journal          Eur. J. Biochem. (1993) 217:45-52
#title            Gene sequence, cDNA construction, expression in Escherichia
#accession        S38373      coli and genetically approached purification of porcine
#status           interleukin-1-beta.
#preliminary      S38373
#molecule_type   DNA
#residues         1-267 #label VAN
#cross-references EMBL:X74568
#introns          16/2; 33/3; 99/1; 154/1; 197/3
#superfamily      interleukin-1
CLASSIFICATION    #length 267 #molecular-weight 29893 #checksum 8512
SUMMARY           Query Match 16.5%; Score 214; DB 6; Length 267;
                   Best Local Similarity 38.5%; Pred. No. 1.60e-20;
                   Matches 30; Conservative 14; Mismatches 33; Indels 1; Gaps 1;

Db 174 lgikgnlyscvmkddtptlqledvdkyp-krdmekrfvfykteknrvfesalyp 232
   ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| |
Oy 86 LGIHGKMLCVKSGDETRQLQLEAVNITDLSNRKQDKRFATIRSDSGPTTSFESAACP 145
   ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| |
Db 233 nwlstsqaeqkpvflgn 250
   ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| |
Oy 146 GWFLCTAMEADQPVSLTN 163
   ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| |

RESULT 12
ENTRY             ICHUIB      #type complete
TITLE             interleukin-1 beta precursor - human
ALTERNATE_NAMES   hematopoietin-1; IL-1 beta
ORGANISM          #formal_name Homo sapiens #common_name man
DATE              28-Feb-1986 #sequence_revision 28-May-1986 #text_change
ACCESSIONS        A25542; A29019; A94023; A93361; B27616; I51852; I65200;
REFERENCE          I38132; A01848; S19626
#authors          Clark, B.D.; Collins, K.L.; Gandy, M.S.; Webb, A.C.; Auron,
#journal          P.E.
#journal          Nucleic Acids Res. (1986) 14:7897-7914
#title            Genomic sequence for human prointerleukin 1 beta: possible
                   evolution from a reverse transcribed prointerleukin 1 alpha
                   gene.
#cross-references MUID:87040762
#accession        A25542
#molecule_type   DNA
#residues         1-269 #label CLA
#cross-references GB:X04500
REFERENCE          A29019
#authors          Bensi, G.; Raugi, G.; Palla, E.; Carinci, V.; Buonamassa,
#journal          D.T.; Melli, M.
#journal          Gene (1987) 52:95-101
#title            Human interleukin-1 beta gene.
#cross-references MUID:87248099
#accession        A29019
#molecule_type   DNA
#residues         1-5, 'E', 7-269 #label BEN
#cross-references GB:M15840
REFERENCE          A94023
#authors          Auron, P.E.; Webb, A.C.; Rosenwasser, L.J.; Mucci, S.F.;
#journal          Rich, A.; Wolff, S.M.; Dinarello, C.A.
#journal          Proc. Natl. Acad. Sci. U.S.A. (1984) 81:7907-7911
#title            Nucleotide sequence of human monocyte interleukin 1 precursor
                   cDNA.
#cross-references MUID:85088517
#accession        A94023
#molecule_type   mRNA
#residues         1-269 #label AUR
#cross-references GB:X02770
REFERENCE          A93361
#authors          March, C.J.; Mosley, B.; Larsen, A.; Cerretti, D.P.; Braedt,
#journal          G.; Price, V.; Gillis, S.; Henney, C.S.; Kronheim, S.R.;
#journal          Grabstein, K.; Conlon, P.J.; Hopp, T.P.; Cosman, D.
#title            Nature (1985) 315:641-647
#accession        MUID:85240547
#cross-references MUID:85240547
#molecule_type   mRNA
#residues         1-5, 'E', 7-269 #label MAR
#cross-references GB:X02532
#note             parts of this sequence, including the amino end of the
                   mature form, were confirmed by peptide sequencing;
                   confirmed absence of glycosylation at 123-Asn
REFERENCE          A90732

```

**Best Available Copy**

#authors Cannon, J.G.; Clark, B.D.; Wingfield, P.; Schweissner, U.;  
 #journal J. Immunol. (1989) 142:2299-2306  
 #title Rabbit IL-1. Cloning, expression, biologic properties, and  
 transcription during endotoxemia.  
 #cross-references MUID:89176242  
 #accession A30584  
 ##molecule\_type mRNA  
 ##residues 1-268 ##label CAN  
 REFERENCE A94230  
 #authors Young, P.R.; Sylvester, D.  
 #journal Protein Eng. (1989) 2:545-551  
 #title Cloning of rabbit interleukin-1 beta: differential evolution  
 of IL-1 alpha and IL-1 beta proteins.  
 #cross-references MUID:89315718  
 #accession JU0082  
 ##molecule\_type mRNA  
 ##residues 1-268 ##label YOU  
 COMMENT This protein lacks a conventional signal sequence for protein  
 export. Cleavage of a long N-terminal propeptide occurs with  
 secretion, although uncleaved forms are also released. The  
 uncleaved form of interleukin-1beta, unlike interleukin 1-alpha,  
 is inactive.  
 COMMENT Interleukin-1beta precursor is less heavily myristoylated than  
 interleukin-1alpha precursor.  
 CLASSIFICATION #superfamily interleukin-1  
 KEYWORDS cytokine; immunoregulation; inflammation; lymphokine;  
 macrophage; mitogen  
 FEATURE 117-268  
 #product interleukin-1 beta #status predicted #label ILB  
 #length 268 #molecular\_weight 30665 #checksum 3461  
 SUMMARY  
 Query Match 15.0%; Score 195; DB 2; Length 268;  
 Best Local Similarity 37.2%; Pred. No. 4.27e-17;  
 Matches 29; Conservative 16; Mismatches 32; Indels 1; Gaps 1;  
 Db 175 lgrgknylscvnmkdkptqlqlesvd-pnryppkkmekrfvfkielekldklesaqfp 233  
 QY 86 LGIHGKMKCLSCVKSGDETRQLQLEAVNITLSENKQKRFIRSDSGPTTSFESAACP 145  
 Db 234 nwyistsqteymvplgn 251  
 QY 146 GWFICTAEADQPVSLN 163

RESULT 14  
 ENTRY #type complete  
 ORGANISM N-acyl-L-amino acid amidohydrolase - Bacillus  
 #formal\_name Bacillus stearothermophilus  
 #formal\_name Bacillus stearothermophilus  
 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change  
 12-Aug-1996  
 ACCESSIONS I40358  
 REFERENCE I40357  
 #authors Sakanyan, V.; Desmarez, L.; Legrain, C.; Charlier, D.; Mett,  
 T.; Kochikyan, A.; Savchenko, A.; Boyen, A.; Falmagne, P.;  
 Pirard, A.; Glansdorff, N.  
 #journal Appl. Environ. Microbiol. (1993) 59:3878-3888  
 #title Gene cloning, sequence analysis, purification, and  
 characterization of a thermostable aminoacylase from  
 Bacillus stearothermophilus.  
 #cross-references MUID:94113715  
 #accession I40358  
 ##status preliminary; translated from GB/EMBL/DBJ  
 ##molecule\_type DNA  
 ##residues 1-370 #label RES  
 ##cross-references EMBL:X74289; NID:g436795; CDS\_PID:g436797  
 GENETICS  
 #gene ama  
 #length 370 #molecular\_weight 41676 #checksum 5132  
 SUMMARY  
 Query Match 7.4%; Score 96; DB 12; Length 370;  
 Best Local Similarity 25.3%; Pred. No. 3.36e-01;

#authors Cannon, J.G.; Clark, B.D.; Wingfield, P.; Schweissner, U.;  
 #journal J. Immunol. (1989) 142:2299-2306  
 #title Rabbit IL-1. Cloning, expression, biologic properties, and  
 transcription during endotoxemia.  
 #cross-references MUID:89176242  
 #accession A30584  
 ##molecule\_type mRNA  
 ##residues 1-268 ##label CAN  
 REFERENCE A94230  
 #authors Young, P.R.; Sylvester, D.  
 #journal Protein Eng. (1989) 2:545-551  
 #title Cloning of rabbit interleukin-1 beta: differential evolution  
 of IL-1 alpha and IL-1 beta proteins.  
 #cross-references MUID:89315718  
 #accession JU0082  
 ##molecule\_type mRNA  
 ##residues 1-268 ##label YOU  
 COMMENT This protein lacks a conventional signal sequence for protein  
 export. Cleavage of a long N-terminal propeptide occurs with  
 secretion, although uncleaved forms are also released. The  
 uncleaved form of interleukin-1beta, unlike interleukin 1-alpha,  
 is inactive.  
 COMMENT Interleukin-1beta precursor is less heavily myristoylated than  
 interleukin-1alpha precursor.  
 CLASSIFICATION #superfamily interleukin-1  
 KEYWORDS cytokine; immunoregulation; inflammation; lymphokine;  
 macrophage; mitogen  
 FEATURE 117-268  
 #product interleukin-1 beta #status predicted #label ILB  
 #length 268 #molecular\_weight 30665 #checksum 3461  
 SUMMARY  
 Query Match 15.0%; Score 195; DB 2; Length 268;  
 Best Local Similarity 37.2%; Pred. No. 4.27e-17;  
 Matches 29; Conservative 16; Mismatches 32; Indels 1; Gaps 1;  
 Db 175 lgrgknylscvnmkdkptqlqlesvd-pnryppkkmekrfvfkielekldklesaqfp 233  
 QY 86 LGIHGKMKCLSCVKSGDETRQLQLEAVNITLSENKQKRFIRSDSGPTTSFESAACP 145  
 Db 234 nwyistsqteymvplgn 251  
 QY 146 GWFICTAEADQPVSLN 163

Matches 20; Conservative 23; Mismatches 30; Indels 6; Gaps 6;  
 Db 64 rli-gqgprvrvairadndalpiqeentfefasknpgvm-hacghdghtaml-lgtakif 120  
 QY 57 QLVAGVLPQPNVNLKIDVPI-EPHAL-FLGIHGKMKCLSCVKSGDETRQLQLEAVNI- 113  
 Db 121 sqldrdirgeirflfqhae 139  
 QY 114 TDLSENKQKRFIRSD 132

RESULT 15  
 ENTRY #type complete  
 TITLE thrombin receptor - rat  
 ORGANISM #formal\_name Rattus norvegicus #common\_name Norway rat  
 DATE 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change  
 16-Feb-1997  
 ACCESSIONS A43448  
 REFERENCE A43448  
 #authors Zhong, C.; Hayzer, D.J.; Corson, M.A.; Runge, M.S.  
 #journal J. Biol. Chem. (1992) 267:16975-16979  
 #title Molecular cloning of the rat vascular smooth muscle thrombin  
 receptor. Evidence for in vitro regulation by basic  
 fibroblast growth factor.  
 #cross-references MUID:92381002  
 #accession A43448  
 ##status preliminary  
 ##molecule\_type mRNA  
 ##residues 1-432 #label ZHO  
 ##cross-references NCBI:111973; NCBI:111974  
 ##experimental\_source RASM aortic smooth muscle cells  
 #note sequence extracted from NCBI backbone  
 G protein-coupled receptor; transmembrane protein  
 #length 432 #molecular\_weight 48280 #checksum 6313  
 SUMMARY  
 Query Match 7.2%; Score 93; DB 16; Length 432;  
 Best Local Similarity 35.0%; Pred. No. 8.33e-01;  
 Matches 14; Conservative 11; Mismatches 14; Indels 1; Gaps 1;  
 Db 43 nprsfllrnp-edtfefpfgdeeknesiplegayvl 81  
 QY 47 NORTFLRNQLVAGYLOGPNVNLEEKIDVVPTEPHALFL 86

Search completed: Thu Feb 19 10:10:36 1998  
 Job time : 30 secs.



\*\*\*\*\*  
M P E R L H  
(TM)  
\*\*\*\*\*

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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Thu Feb 19 10:10:54 1998; MasPar time 5.54 Seconds  
689.392 Million cell updates/sec  
No output not generated.

Title: >US-08-910-733-13  
Description: (1-180) from US08910733.pep  
Perfect Score: 1298  
Sequence: 1 MALADLYEKGGGGGEGEDN.....LTNMPDEGVMVTKFYQEDE 180

Scoring table: PAM 150  
Gap 11

Searched: 59021\_seqs, 21210388 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot34  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 43.764; Variance 70.225; scale 0.623

Pred.. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	ID	Description	Pred. No.
1	1140	87.8	177	5	IL1X_HUMAN INTERLEUKIN-1 RECEPTO	1.48e-256
2	965	74.3	177	5	IL1X_RABIT INTERLEUKIN-1 RECEPTO	4.31e-211
3	955	73.6	178	5	IL1X_MOUSE INTERLEUKIN-1 RECEPTO	1.67e-208
4	905	69.7	178	5	IL1X_RAT INTERLEUKIN-1 RECEPTO	1.39e-195
5	230	17.7	269	5	IL1B_MOUSE INTERLEUKIN-1 BETA PR	1.85e-28
6	229	17.6	266	5	IL1B_BOVIN INTERLEUKIN-1 BETA PR	3.09e-28
7	228	17.6	266	5	IL1B_SHEEP INTERLEUKIN-1 BETA PR	5.13e-28
8	223	17.2	266	5	IL1B_CEREL INTERLEUKIN-1 BETA PR	6.50e-27
9	205	15.8	267	5	IL1B_PIG INTERLEUKIN-1 BETA PR	5.41e-23
10	202	15.6	269	5	IL1B_MACMU INTERLEUKIN-1 BETA PR	2.39e-22
11	202	15.6	269	5	IL1B_MACNE INTERLEUKIN-1 BETA PR	2.39e-22
12	200	15.4	269	5	IL1B_HUMAN INTERLEUKIN-1 BETA PR	6.42e-22
13	198	15.3	267	5	IL1B_FELCA INTERLEUKIN-1 BETA PR	1.72e-21
14	195	15.0	268	5	IL1B_RABIT INTERLEUKIN-1 BETA PR	7.49e-21
15	184	14.2	269	5	IL1B_CERTO INTERLEUKIN-1 BETA PR	1.57e-18
16	96	7.4	370	1	AMA_BACST N-ACYL-L-AMINO ACID A	5.25e-02
17	93	7.2	432	9	THRR_RAT THROMBIN RECEPTOR PRE	1.51e-01
18	92	7.1	1024	10	Y075_MYCGE HYPOTHETICAL PROTEIN	2.14e-01
19	89	6.9	320	9	SOX2_SHEEP SOX-2 PROTEIN	5.97e-01
20	89	6.9	396	3	EFTU_FLESI ELONGATION FACTOR TU	5.97e-01
21	89	6.9	795	3	ENPL_CHICK ENDOPLASMIN PRECURSOR	5.97e-01
22	88	6.8	157	11	Y117_YEAST HYPOTHETICAL 16.9 KD	8.35e-01

RESULT	ID	IL1X_HUMAN	STANDARD;	PRT;	177 AA.
AC	P18510;				
DT	01-NOV-1990	(REL. 16, CREATED)			
DT	01-NOV-1990	(REL. 16, LAST SEQUENCE UPDATE)			
DT	01-FEB-1996	(REL. 33, LAST ANNOTATION UPDATE)			
DE	INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (ICIL-1RA) (IRAP).				
GN	IL1RN OR IL1RA.				
OS	HOMO SAPIENS (HUMAN).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; PRIMATES.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 90220867.				
RA	CARTER D.B., DEIBEL M.R. JR., DUNN C.J., TOMICH C.S.C., LABORDE A.L., SLIGHTOM J.L., BERGER A.E., BIENKOWSKI M.J., SUN F.F., MCEWAN R.N., HARRIS P.K.W., YEM A.W., WASZAK G.A., CHOSAY J.G., SIEU L.C., HARDEE M.M., ZURCHER-NEELY H.A., REARDON I.M., HEINRIKSON R.L., TRUESDELL S.E., SHELLY J.A., EESSALU T.E., TAYLOR B.M., TRACEY D.E.; NATURE 344:633-638(1990).				
RL	NATURE 344:633-638(1990).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 90136921.				
RA	EISENBERG S.P., EVANS R.J., AREND W.P., VERDERBER E., BREWER M.T., HANNUM C.H., THOMPSON R.C.; NATURE 343:341-346(1990).				
RL	NATURE 343:341-346(1990).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 91271363.				
RA	EISENBERG S.P., BREWER M.T., VERDERBER E., HEIMDAL P., BRANDHUBER B.J., THOMPSON R.C.; PROC. NATL. ACAD. SCI. U.S.A. 88:5232-5236(1991).				
RL	PROC. NATL. ACAD. SCI. U.S.A. 88:5232-5236(1991).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 92338323.				
RA	LENNARD A., GORMAN P., CARRIER M., GRIFFITHS S., SCOTNEY H., SHEER D., SOLARI R.; CYTOKINE 4:83-89(1992).				
RL	CYTOKINE 4:83-89(1992).				
RN	[5]				
RP	SEQUENCE OF 26-45.				
RX	MEDLINE; 90136920.				
RA	HANNUM C.H., WILCOX C.J., AREND W.P., JOSLIN F.G., DRIPPS D.J., HEIMDAL P.L., ARMES L.G., SOMMER A., EISENBERG S.P., THOMPSON R.C.; NATURE 343:336-340(1990).				
RL	NATURE 343:336-340(1990).				
RN	[6]				

ALIGNMENTS

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85 FLGIHGGKMLSCVKSGBDETRQLQLEAVNITDLSENRKQDKRFAFRSDSGPTTSFESAAC 144

142 pgwfictameadqpsvsltnmpdegvmvkfyfgede 177
|||||
145 PGWFELCTAMEADQPVSILTNMPDEGYMVKFYFEDE 180

RESULT 2
ILIX RABIT STANDARD; PRT; 177 AA.
P26890;
01-AUG-1992 (REL. 23, CREATED)
01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (IL-1RN)
(IRAPL).
OS ORYCTOLAGUS CUNICULUS (RABBIT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EC EUTHERIA; LAGOMORPHA.
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 94165101.
RA COMINELLI F., BORTOLAMI M., PIZARRO T.T., MONSACCHI L., FERRETTI M.,
RW BREWER M.T., EISENBERG S.P.; NG R.K.;
RL J. BIOL. CHEM. 269:6962-6971(1994).
[2]
RN SEQUENCE FROM N.A.
RW HAMADA H., MULLIGAN R.C.;
RL SUBMITTED (XX-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
[3]
RN SEQUENCE FROM N.A.
RX MEDLINE: 93052512.
RA GOTO F., GOTO K., MIYATA T., OHKAWARA S., TAKAO T., MORI S.,
RW FURUKANA S., MAEDA T., IWANAGA S., SHIMONISHI Y., YOSHINAGA M.;
RL IMMUNOLOGY 77:235-244(1992).
CC -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CCC RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CCC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
DR EMBL; S68977; G545741; -
DR EMBL; M57526; G165437; -
DR EMBL; D21832; G452205; -
DR PIR; A54377; A54377.
DR HSSP; P18510; IILR.
DR PROSITE; PS00253; INTERLEUKIN_1.
KW GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 25 BY SIMILARITY.
FT CHAIN 26 177 INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT FT PROTEIN.
CARBOHYD 109 109 POTENTIAL.
SEQUENCE 177 AA; 20214 MW; DD97CDC2 CRC32;

Query Match 74.3%; Score 965; DB 5; Length 177;
Best Local Similarity 78.2%; Pred. No. 4.3le-21l;
Matches 122; Conservative 24; Mismatches 10; Indels 0; Gaps 0;

Db 22 etacrspgkrcmcafiwdvngktftlrnqlvagylvqqgnakleeridvvplepqll 81
||| |||::: :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 25 ETICRPSPGRKSKGMQAFRIWDVNQKTFYLRNNQLVAGLVQGPNVLKEIDVVPPIEPHAL 84
||||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 82 fligrgklclscvksvgdkmkhlheavnitdlgnkegdkrftfirnsqpgtttffesasc 141
|||| |:||| ||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 85 FLGIHGGKMLSCVKSGBDETRQLQLEAVNITDLSENRKQDKRFAFRSDSGPTTSFESAAC 144

Db 142 pgwfictaleadqpsvsltnptdsvvvtkfkyfqedq 177
|||||
QY 145 PGWFELCTAMEADQPVSILTNMPDEGYMVKFYFEDE 180

RESULT 3
ILIX MOUSE STANDARD; PRT; 178 AA.
P25085;
01-MAY-1992 (REL. 22, CREATED)
01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)

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01-NOV-1995 (REL 32, LAST ANNOTATION UPDATE)
INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (IL-IRN)
(IRAP).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
[1] SEQUENCE FROM N.A.
RN RNP SEQENCE FROM N.A.
RP MEDLINE: 91250712.
RR ZAHEDI K., SELDIN M.F., RITS M., EZEKOWITZ R.A., WHITEHEAD A.S.;
RRA J. IMMUNOL. 146:4228-4233(1991).
RN [2]
RN RNP SEQUENCE FROM N.A.
RX MEDLINE: 91316273.
RXX MATSUSHIME H., ROUSSEL M.F., MATSUSHIMA K., HISHINUMA A., SHERR C.J.;
RRL BLOOD 78:616-623(1991).
RN [3]
RN RNP SEQUENCE FROM N.A.
RP STRAIN-SWISS;
RR MEDLINE: 94271931.
RFX ZAHEDI K.A., UHLAR C.M., RITS M., PRADA A.E., WHITEHEAD A.S.;
RRR CYTOKINE 6:1-9(1994).
RN [4]
RN RNP SEQUENCE OF 7-178 FROM N.A.
RP MEDLINE: 91271363.
RXX EISENBERG S.P., BREWER M.T., VERDERBER E., HEIMDAL P.,
RRA BRANDHUBER B.J., THOMPSON R.C.;
RRL PROC. NATL. ACAD. SCI. U.S.A. 88:5232-5236(1991).
RN [5]
RN RNP SEQUENCE OF 23-178 FROM N.A.
RP MEDLINE: 92037824.
RXX SHUCK M.E., BESSAU T.E., TRACEY D.E., BIENKOWSKI M.J.;
RRA EUR. J. IMMUNOL. 21:2775-2780(1991).
CCC -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CCC RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CCC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
EMBL; M74294; G198388; -
EMBL; M64404; G198297; -
EMBL; L32838; G528978; -
EMBL; M57525; G198299; -
EMBL; M63100; G198390; -
EMBL; M64082; G238585; -
PIR; B40956; B40956.
PIR; A44610; A44610.
HSP; P18510; IILR.
PROSITE; PS00253; INTERLEUKIN_1.
GLYCOPROTEIN; SIGNAL.
SIGNAT 1 26 BY SIMILARITY.
CHAIN 27 178 INTERLEUKIN-1 RECEPTOR ANTAGONIST
POTENTIAL.
CARBOHYD 110 110
SEQUENCE 178 AA; 20274 MW; 687FEA9 CRC32;
Query Match 73.6%; Score 955; DB 5; Length 178;
Best Local Similarity 76.3%; Pred. No. 1.67e+208;
Matches 119; Conservative 25; Mismatches 12; Indels 0; Gaps 0;
Ddb 23 eaacrpgrckmqafriwdnqkftfrrnnqlagylggnpnkleekidmvpdlhsv 82
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 25 FTICPRSSKKMQAFRIWDNYNTFTYLNNQLVAGLVGGPNVLEEKIDVVPFEPHAL 84
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Ddb 83 flighggklclscaksgddiklqeavnidtsknkeedkrftfirsekgttfsesaa 142
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 85 FLGIHGKNMCLSCVSGDETRIQLEAVNIITDSENRKDQRFAFRISDSGPPTSESAAC 144
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Ddb 143 pgwfcittleadrpsvlntptpeelivtkfyfqgd 178
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 145 PGWFCLTAEEADQPVSLTNWPDGVGWTKFYQEDE 180

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AC	P25086;
DT	01-MAY-1992 (REL. 22, CREATED)
DE	01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DE	01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE	INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (IL-IRN)
DE	(IRAP)
GN	IL1RN OR IL-1RA.
OS	RATTUS NORVEGICUS (RAT).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; RODENTIA.
[1]	
RN	SEQUENCE FROM N.A.
RP	MEDLINE; 91271363.
RX	EISENBERG S.P., BREWER M.T., VERDERBER E., HEIMDAL P.,
RA	BRANDHUBER B.J., THOMPSON R.C.;
RA	PROC. NATL. ACAD. SCI. U.S.A. 88:5232-5236(1991).
RL	- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC	RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC	- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC	EMBL; M63101; G204929; -;
DR	PIR; C40956; C40956.
DR	HSSP; P18510; 1ILR.
DR	PROSITE; PS00253; INTERLEUKIN_1.
KW	GLYCOPROTEIN; SIGNAL.
FT	SIGNAL 1 26
FT	CHAIN 27 178
FT	POTENTIAL.
FT	INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT	PROTEIN.
FT	CARBOHYD 110 110
FT	SEQUENCE 178 AA; 20282 MW; 80AE76EC CRC32;
FT	Query Match 69.7%; Score 905; DB 5; Length 178;
FT	Best Local Similarity 73.7%; Pred. No. 1.39e-195;
FT	Matches 115; Conservative 25; Mismatches 16; Indels 0; Gaps
DB	23 esaghpagrkpcmkqafriwdntngktfyrlnnqlagiylggnptkleeidmvpdfrnv 82
QY	I : :::::
QY	25 ETFCRCPSKSKMQAFRIWDNYNQKTFYLRNNQLVAGYLQGPNVLKEEKIDVVPPEHAL 84
DB	83 fgihgkgklcslcvsgddtklgleevnitdknkkeedkrftfirsetgpptsfeslac 142
QY	F I I H G G K W C L S C V S G D F T R L Q L E A V N I T D L S E N R K Q D K R F A F I R S D S G P T T S F E S A A C 144
DB	143 pgwficttiieadhpvsltntpkcpctvkfyfqgd 178
QY	:
QY	145 PGWFCLTAMEADQPVSILTNPMDGVMTKFYFQEDE 180
RESULT	5
ID	IL1B.MOUSE STANDARD; PRT: 269 AA.
AC	P10749;
DT	01-JUL-1989 (REL. 11, CREATED)
DT	01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
DT	01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE	INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
GN	IL1B.
OS	MUS MUSCULUS (MOUSE).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; RODENTIA.
[1]	
RN	SEQUENCE FROM N.A.
RP	MEDLINE; 87058957.
RX	GRAY P.W., GLAISTER D., CHEN E., GOEDEL D.V., PENNICCA D.;
RL	J. IMMUNOL. 137:3644-3648(1986).
RL	[2]
RN	SEQUENCE FROM N.A.
RP	MEDLINE; 87117546.
RX	TELFORD J.L., MACCHIA G., MASSONE A., CARINCI V., PALLA E., MELLI M.;
RL	NUCLEIC ACIDS RES. 14:9955-9963(1986).
RL	[3]
RN	SEQUENCE OF 118-139.
RX	MEDLINE; 88229074.
RX	HUANG J.J., NEWTON R.C., RUTLEDGE S.J., HORUK R., MATTHEW J.B.,
RA	COVINGTON M., LIN Y.:

RL J. IMMUNOL. 140:3838-3843(1988).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RA MEDLINE:82222282  
 RX VAN OOSTRUM J., PRIESTLE J.P., GRUTTER M.G., SCHMITZ A.;  
 RL J. STRUCT. BIOL. 107:189-195(1991).  
 CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES  
 CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL  
 CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.  
 CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING  
 CC IDENTIFIED AS ENDOGENOUS PYROGEN, AND ARE REPORTED TO STIMULATE  
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNIOVAL CELLS.  
 CC -!- SUBUNIT: MONOMER.  
 CC -!- THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO  
 CC ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.  
 CC -!- THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR  
 CC SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS  
 CC SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER  
 CC SECRETORY PROTEINS.  
 CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.  
 DR EMBL; M15131; G309398; -.  
 DR EMBL; X04964; G52667; -.  
 DR PIR; A24719; A24719.  
 DR PIR; S13029; S13029.  
 DR PDB; 811B; 15-OCT-94.  
 DR PDB; 2M1B; 31-JAN-94.  
 DR PROSITE; PS00253; INTERLEUKIN\_1.  
 KW CYTOKINE; MACROPHAGE; MITOGEN; INFLAMMATORY RESPONSE; PYROGEN;  
 KW 3D-STRUCTURE.  
 FT PROPEP 1 117  
 FT CHAIN 118 269 INTERLEUKIN-1 BETA.  
 FT CARBOHYD 57 57  
 FT CARBOHYD 253 253 POTENTIAL.  
 FT STRAND 123 129  
 FT TURN 130 131  
 FT STRAND 134 137  
 FT TURN 140 141  
 FT STRAND 143 146  
 FT TURN 150 154  
 FT STRAND 159 163  
 FT TURN 170 171  
 FT STRAND 173 179  
 FT TURN 180 181  
 FT STRAND 184 191  
 FT TURN 192 193  
 FT STRAND 194 201  
 FT TURN 204 206  
 FT HELIX 214 216  
 FT STRAND 217 222  
 FT STRAND 227 231  
 FT TURN 235 236  
 FT STRAND 238 242  
 FT STRAND 247 248  
 FT STRAND 250 252  
 FT STRAND 258 259  
 FT STRAND 262 266  
 SQ SEQUENCE 269 AA; 30931 MW; B72ACA9F CRC32;  
 Query Match 17.78; Score 230; DB 5; Length 269;  
 Best Local Similarity 30.79; Pred. No. 1.85e-28;  
 Matches 42; Conservative 34; Mismatches 53; Indels 8; Gaps 7;  
 Db 125 ylrdeqkxslvdpyelkallhngqniqqvifmsfvqgpepsndkipvalgkqknl 184  
 QY 41 FRWDVYQKTFYLRNN-QLVAGYLGQPNVLEKIDV--VPIEP-HA-L-F-LGIHGGKM 93  
 Db 185 ylsvcnkdgtptlqlesvdpkqyp-kkkmekrfvfnkievskvfeafnwyistsq 243  
 QY 94 CLSCVKSGDETRQLQEAVNITDLSENKQDKRFARISDSGPTTSFESAACPGWFLCTAM 153  
 Db 244 aebkpfvlgnsqgdii 260  
 QY 154 EADQPVSLTNMPDEGM 170

RESULT 6  
 ID IL1B\_BOVIN STANDARD; PRT; 266 AA.  
 AC P09428;  
 DT 01-MAR-1989 (REL. 10, CREATED)  
 DT 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
 DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).  
 GN IL1B.  
 OS BOS TAURUS (BOVINE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; ARTIODACTYLA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 89016591.  
 RA LEONG S.R., FLAGGS G.M., LAWMAN M., GRAY P.W.;  
 RL NUCLEIC ACIDS RES. 16:9054-9054(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 88318652.  
 RA MALISZEWSKI C.R., BAKER P.E., SCHOENBORN M.A., DAVIS B.S., COSMAN D.,  
 RA GILLIS S., CERRETTI D.P.;  
 RL MOL. IMMUNOL. 25:429-437(1988).  
 CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES  
 CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL  
 CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.  
 CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING  
 CC IDENTIFIED AS ENDOGENOUS PYROGEN, AND ARE REPORTED TO STIMULATE  
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNIOVAL CELLS.  
 CC -!- SUBUNIT: MONOMER.  
 CC -!- THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO  
 CC ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.  
 CC -!- THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR  
 CC SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS  
 CC SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER  
 CC SECRETORY PROTEINS.  
 CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.  
 DR EMBL; M35589; G163203; -.  
 DR EMBL; X12498; G449; -.  
 DR EMBL; M37211; G163201; -.  
 DR PIR; JL0010; ICB01B.  
 DR PIR; S01380; S01380.  
 DR HSP; P01584; IHI1B.  
 DR PROSITE; PS00253; INTERLEUKIN\_1.  
 KW CYTOKINE; MACROPHAGE; MITOGEN; INFLAMMATORY RESPONSE; PYROGEN.  
 FT PROPEP 1 113  
 FT CHAIN 114 266 INTERLEUKIN-1 BETA.  
 FT CARBOHYD 58 58 POTENTIAL.  
 FT CONFLICT 252 252 A -> G (IN REF. 2).  
 SQ SEQUENCE 266 AA; 30774 MW; 1DF2785C CRC32;  
 Query Match 17.68; Score 229; DB 5; Length 266;  
 Best Local Similarity 37.18; Pred. No. 3.09e-28;  
 Matches 33; Conservative 17; Mismatches 37; Indels 2; Gaps 2;  
 Db 173 lgikdknlylscvkkqgdtpqlqleevd-pkvyppkrnmekrfvfykltelkntvefsvlyp 231  
 QY 86 LGIHGGKMLSCVKSQSGDETRQLQEAVNITDLSENKQDKRFARISDSGPTTSFESAACP 145  
 Db 232 nwyistsqleerpfvlfghfra-gqditdf 259  
 QY 146 GWFLCTAMEADQPVSLTNMPDEGMVTKF 174  
 RESULT 7  
 ID IL1B\_SHEEP STANDARD; PRT; 266 AA.  
 AC P21621;  
 DT 01-MAY-1991 (REL. 18, CREATED)  
 DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
 DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).  
 GN IL1B.

OS OVIS ARIES (SHEEP).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 RN EUTHERIA; ARTIODACTYLA.  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 92119335.  
 RA SEOW H.F., ROTHSEL J.S., DAVID M.J., WOOD P.R.;  
 RL DNA SEQ. 1:423-426(1991).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 91088326.  
 RA FISKESTRAND C., SARGAN D.;  
 RL NUCLEIC ACIDS RES. 18:7165-7165(1990).  
 CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES  
 CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL  
 CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.  
 CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING  
 CC IDENTIFIED AS ENDOGENOUS PYROGEN, AND ARE REPORTED TO STIMULATE  
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNIOVAL CELLS.  
 CC -!- SUBUNIT: MONOMER.  
 CC -!- THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO  
 CC ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.  
 CC -!- THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR  
 CC SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS  
 CC SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER  
 CC SECRETORY PROTEINS.  
 CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.  
 CC EMBL: X54796; G1274; -  
 DR EMBL: X56972; G1809; -  
 DR PIR: S13092; S13092.  
 DR PIR: S13810; S13810.  
 DR PIR: S23010; S23010.  
 DR HSSP: P01584; 1HIB.  
 DR PROSITE: PS00253; INTERLEUKIN-1.  
 KW CYTOKINE; MACROPHAGE; MITOGEN; INFLAMMATORY RESPONSE; PYROGEN.  
 FT PROPEP 1 113  
 FT CHAIN 114 266 INTERLEUKIN-1 BETA.  
 FT CARBOHYD 58 58 POTENTIAL.  
 FT CONFLICT 14 14 Y > C (IN REF. 2).  
 FT CONFLICT 55 55 Q > K (IN REF. 2).  
 FT CONFLICT 64 64 V > A (IN REF. 2).  
 FT CONFLICT 145 145 P > L (IN REF. 2).  
 SQ SEQUENCE 266 AA; 304717 MW; 0BD99138 CRC32;  
 Query Match 17.6%; Score 228; DB 5; Length 266;  
 Best Local Similarity 37.1%; Pred. No. 5,13e-28;  
 Matches 33; Conservative 16; Mismatches 38; Indels 2; Gaps 2;  
 Db 173 lgirdknlyscvkkgtptlqlleevd-pkvyprkrmekrfvfyktelkntvesfslp 231  
 Qy 86 LGHGGKMLCSVKSGDETQLQLEAVNITDLSENKQDKRFAFIRSDSGPTTSFESAACP 145  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 93314975.  
 RA HUTHER M.J., LIN G., SMITH D.M., MURTAUGH M.P., MOLITOR T.W.;  
 RL GENE 129:285-289(1993).  
 CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES  
 CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL  
 CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.  
 CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING  
 CC IDENTIFIED AS ENDOGENOUS PYROGEN, AND ARE REPORTED TO STIMULATE  
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNIOVAL CELLS.  
 CC -!- SUBUNIT: MONOMER.  
 CC -!- THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO  
 CC ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.  
 CC -!- THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR  
 CC SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS  
 CC SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER  
 CC SECRETORY PROTEINS.  
 CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.  
 CC EMBL: M86725; G164608; -  
 DR PIR: JN0724; JN0724.  
 DR HSSP: P01584; 1HIB.  
 DR PROSITE: PS00253; INTERLEUKIN-1.  
 KW CYTOKINE; MACROPHAGE; MITOGEN; INFLAMMATORY RESPONSE; PYROGEN.  
 FT PROPEP 1 114  
 FT CHAIN 115 267 INTERLEUKIN-1 BETA.  
 FT CARBOHYD 46 46 POTENTIAL.  
 FT CARBOHYD 59 59 POTENTIAL.  
 SQ SEQUENCE 267 AA; 30404 MW; 5930DFAB CRC32;  
 Query Match 17.2%; Score 223; DB 5; Length 266;  
 Best Local Similarity 37.1%; Pred. No. 6,50e-27;  
 Matches 33; Conservative 16; Mismatches 38; Indels 2; Gaps 2;  
 Db 173 lgirdknlyscvkkgtptlqlleevd-pkvyprkrmekrfvfyktelkntvesfslp 231  
 Qy 86 LGHGGKMLCSVKSGDETQLQLEAVNITDLSENKQDKRFAFIRSDSGPTTSFESAACP 145  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 93314975.  
 RA HUTHER M.J., LIN G., SMITH D.M., MURTAUGH M.P., MOLITOR T.W.;  
 RL GENE 129:285-289(1993).  
 CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES  
 CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL  
 CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.  
 CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING  
 CC IDENTIFIED AS ENDOGENOUS PYROGEN, AND ARE REPORTED TO STIMULATE  
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNIOVAL CELLS.  
 CC -!- SUBUNIT: MONOMER.  
 CC -!- THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO  
 CC ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.  
 CC -!- THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR  
 CC SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS  
 CC SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER  
 CC SECRETORY PROTEINS.  
 CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.  
 CC EMBL: M86725; G164608; -  
 DR PIR: JN0724; JN0724.  
 DR HSSP: P01584; 1HIB.  
 DR PROSITE: PS00253; INTERLEUKIN-1.  
 KW CYTOKINE; MACROPHAGE; MITOGEN; INFLAMMATORY RESPONSE; PYROGEN.  
 FT PROPEP 1 114  
 FT CHAIN 115 267 INTERLEUKIN-1 BETA.  
 FT CARBOHYD 46 46 POTENTIAL.  
 FT CARBOHYD 59 59 POTENTIAL.  
 SQ SEQUENCE 267 AA; 30404 MW; 5930DFAB CRC32;

CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL  
 CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.  
 CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING  
 CC IDENTIFIED AS ENDOGENOUS PYROGEN, AND ARE REPORTED TO STIMULATE  
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNIOVAL CELLS.  
 CC -!- SUBUNIT: MONOMER.  
 CC -!- THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO  
 CC ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.  
 CC -!- THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR  
 CC SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS  
 CC SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER  
 CC SECRETORY PROTEINS.  
 CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.  
 CC EMBL: U20500; G665946; -  
 DR CYTOKINE; MACROPHAGE; MITOGEN; INFLAMMATORY RESPONSE; PYROGEN.  
 FT PROPEP 1 113  
 FT CHAIN 114 266 INTERLEUKIN-1 BETA.  
 FT CARBOHYD 58 58 POTENTIAL.  
 SQ SEQUENCE 266 AA; 30629 MW; 73B32589 CRC32;  
 Query Match 17.2%; Score 223; DB 5; Length 266;  
 Best Local Similarity 37.1%; Pred. No. 6,50e-27;  
 Matches 33; Conservative 16; Mismatches 38; Indels 2; Gaps 2;  
 Db 173 lgirdknlyscvkkgtptlqlleevd-pkvyprkrmekrfvfyktelkntvesfslp 231  
 Qy 86 LGHGGKMLCSVKSGDETQLQLEAVNITDLSENKQDKRFAFIRSDSGPTTSFESAACP 145  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 93314975.  
 RA HUTHER M.J., LIN G., SMITH D.M., MURTAUGH M.P., MOLITOR T.W.;  
 RL GENE 129:285-289(1993).  
 CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES  
 CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL  
 CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.  
 CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING  
 CC IDENTIFIED AS ENDOGENOUS PYROGEN, AND ARE REPORTED TO STIMULATE  
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNIOVAL CELLS.  
 CC -!- SUBUNIT: MONOMER.  
 CC -!- THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO  
 CC ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.  
 CC -!- THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR  
 CC SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS  
 CC SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER  
 CC SECRETORY PROTEINS.  
 CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.  
 CC EMBL: M86725; G164608; -  
 DR PIR: JN0724; JN0724.  
 DR HSSP: P01584; 1HIB.  
 DR PROSITE: PS00253; INTERLEUKIN-1.  
 KW CYTOKINE; MACROPHAGE; MITOGEN; INFLAMMATORY RESPONSE; PYROGEN.  
 FT PROPEP 1 114  
 FT CHAIN 115 267 INTERLEUKIN-1 BETA.  
 FT CARBOHYD 46 46 POTENTIAL.  
 FT CARBOHYD 59 59 POTENTIAL.  
 SQ SEQUENCE 267 AA; 30404 MW; 5930DFAB CRC32;

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 EUTHERIA; PRIMATES.  
 [1]  
 SEQUENCE FROM N.A.  
 TISSUE=BLOOD;  
 MEDLINE: 96003435.  
 VILLINGER F.J., BRAR S.S., MAYNE A.E., CHIKKALA N., ANSARI A.A.;  
 J. IMMUNOL. 155:3946-3954(1995).  
 -!- THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL  
 MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.  
 IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING  
 IDENTIFIED AS ENDOGENOUS PYROGEN, AND ARE REPORTED TO STIMULATE  
 THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.  
 -!- SUBUNIT: MONOMER.  
 -!- THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO  
 ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.  
 -!- THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR  
 SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS  
 SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER  
 SECRETORY PROTEINS.  
 -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.  
 EMBL: U19853; G644824; -  
 CYTOKINE; MACROPHAGE; MITOGEN; INFLAMMATORY RESPONSE; PYROGEN.  
 PROPEP 1 116 BY SIMILARITY.  
 CHAIN 117 269 INTERLEUKIN-1 BETA.  
 SEQUENCE 269 AA; 30612 MW; 30E237F3 CRC32;  
 Query Match 15.6%; Score 202; DB 5; Length 269;  
 Best local Similarity 33.7%; Pred. No. 2.39e-22;  
 Matches 31; Conservative 18; Mismatches 41; Indels 2; Gaps  
 176 lqlaknlyscvldkptqlgslvdpknyp-kkkmekrfvfknieinnklefsaqfp 234  
 86 LGIHGKMLCSVKSGDETRQLQLEAVNTLDSENKQKDFAFIRSDSGPTTSFESAACP 145  
 235 nvyistsgaenmpvfllgtrg-qgditdfmq 265  
 146 GWFELCTMEADQPVSLTNMPDEGVWTKFYFQ 177  
 RESULT 12  
 IL1B\_HUMAN STANDARD; PRT; 269 AA.  
 P01584;  
 21-JUL-1986 (REL. 01, CREATED)  
 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
 INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA) (CATABOLIN).  
 IL1B.  
 HOMO SAPIENS (HUMAN).  
 EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 EUTHERIA; PRIMATES.  
 [1]  
 SEQUENCE FROM N.A.  
 MEDLINE: 85088517.  
 AURON P.E., WEBB A.C., ROSENWASSER L.J., MUCCI S.F., RICH A.,  
 WOLFE S.M., DINARELLO C.A.;  
 PROC. NATL. ACAD. SCI. U.S.A. 81:7907-7911(1984).  
 [2]  
 SEQUENCE FROM N.A.  
 MEDLINE: 85240547.  
 MARCH C.J., MOSLEY B., LARSEN A., CERRETTI D.P., BRAEDT G., PRICE V.,  
 GILLIS S., HENNEY C.S., KRONHEIM S.R., GRABSTEIN K., CONLON P.J.,  
 HOPP T.P., COSMAN D.;  
 NATURE 315:641-647(1985).  
 [3]  
 SEQUENCE FROM N.A.  
 MEDLINE: 87040762.  
 CLARK B.D., COLLINS K.L., GANDY M.S., WEBB A.C., AURON P.E.;  
 NUCLEIC ACIDS RES. 14:7897-7914(1986).  
 [4]  
 SEQUENCE FROM N.A.  
 MEDLINE: 87248099.

BENSI G., RAUGEI G., PALLA E., CARINCI V., BUONAMASSA D.T., MELLI M.  
GENE 52:95-101(1987).  
[5]  
SEQUENCE FROM N.A.  
RX MEDLINE: 90249285.  
RA EMEL'YANOV A.A., KOLLOV A.P., KONSOVA V.G., KOTOV A.X.,  
KURBATOVA T.V., RESHETNIKOV V.L., SIMBIRTSEV S.A., KETLINSKII S.A.,  
VINETSKII Y.P.;  
RA DOKL. AKAD. NAUK SSSR 309:1005-1008(1989).  
[6]  
SEQUENCE FROM N.A.  
RA WEBB A.C., DINARELLO C.A., ROSENWASSER L.J., MUCCI S.F., RICH A.,  
WOLFF S.M., AURON P.E.;  
RA ADV. GENE TECHNOL. 22:339-340(1985).  
[7]  
SEQUENCE FROM N.A.  
RX MEDLINE: 87156769.  
RA NISHIDA T., NISHINO N., TAKANO M., KAWAI K., BANDO K., MASUI Y.,  
NAKAI S., HIRAI Y.;  
RA BIOCHEM. BIOPHYS. RES. COMMUN. 143:345-352(1987).  
[8]  
SEQUENCE OF 117-128.  
RX MEDLINE: 88184226.  
RA ZSEBO K.M., WIPICH J., YUSCHENKOFF V.N., LU H., HUNT P., DUKES P.P.,  
LANGLEY K.E.;  
RA BLOOD 71:962-968(1988).  
[9]  
X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).  
RX MEDLINE: 88211543.  
RA PRIESTLE J.P., SCHAR H.-P., GRUTTER M.G.;  
RA EMBO J. 7:339-343(1988).  
[10]  
X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RX MEDLINE: 90099325.  
RA PRIESTLE J.P., SCHAR H.-P., GRUTTER M.G.;  
RA PROC. NATL. ACAD. SCI. U.S.A. 86:9667-9671(1989).  
[11]  
X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RX MEDLINE: 90064532.  
RA FINZEL B.C., CLANCY L.L., HOLLAND D.R., MUCHMORE S.W.,  
WATENPAUGH K.D., EINSPIER H.M.;  
RA J. MOL. BIOL. 209:779-791(1989).  
[12]  
STRUCTURE BY NMR.  
RX MEDLINE: 90321925.  
RA DRISCOLL P.C., GRONENBORN A.M., WINGFIELD P.T., CLORE G.M.;  
RA BIOCHEMISTRY 29:4668-4682(1990).  
[13]  
STRUCTURE BY NMR.  
RA MEDLINE: 91159409.  
RA CLORE G.M., WINGFIELD P.T., GRONENBORN A.M.;  
RA BIOCHEMISTRY 30:2315-2323(1991).  
CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES  
CC MATURATION & PROLIFERATION, BY INDUCING IL-2 RELEASE, B-CELL  
CC THYMOCYTE PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.  
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING  
CC IDENTIFIED AS ENDOGENOUS PYROGEN, AND ARE REPORTED TO STIMULATE  
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNIOVAL CELLS.  
CC -!- SUBUNIT: MONOMER.  
CC -!- THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO  
CC ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.  
CC -!- THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR  
CC SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS  
CC SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER  
CC SECRETORY PROTEINS.  
CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.  
CC EMBL: M15840; G386816; -  
CC EMBL: X02532; G33790; -  
CC EMBL: K02770; G307043; -  
CC EMBL: X04500; G312408; -  
CC EMBL: X56087; G35663; -  
CC EMBL: M54933; G186288; -

DR	EMBL; M15330; G307045; -
DR	PIR; A01848; ICHULB.
DR	PIR; A25542; A25542.
DR	PIR; A29019; A29019.
DR	PIR; B27616; B27616.
DR	PIR; S19626; S19626.
DR	PDB; 1IIB; 15-OCT-92.
DR	PDB; 2IIB; 15-JUL-93.
DR	PDB; 4IIB; 15-JAN-93.
DR	PDB; 5IIB; 15-OCT-94.
DR	PDB; 6IIB; 15-OCT-92.
DR	PDB; 7IIB; 15-OCT-92.
DR	PDB; 2IBI; 15-APR-92.
DR	PDB; 3IBI; 15-APR-92.
DR	PDB; 4IBI; 15-JUL-92.
DR	PDB; 1HIB; 31-JAN-94.
DR	MIM; 147720; -
DR	PROSITE; PS00253; INTERLEUKIN_1.
KW	CYTOKINE; MACROPHAGE; MITOGEN; INFLAMMATORY RESPONSE; PYROGEN;
KW	3D-STRUCTURE.
FT	PROPEP 1 116
FT	CHAIN 117 269
FT	CARBOHYD 123 123
FT	CONFLICT 6 6
FT	CONFLICT 20 20
FT	CONFLICT 111 111
FT	CONFLICT 177 177
FT	CONFLICT 214 214
FT	CONFLICT 121 128
FT	TURN 129 130
FT	STRAND 132 138
FT	TURN 139 140
FT	STRAND 141 147
FT	TURN 148 150
FT	STRAND 151 151
FT	STRAND 158 162
FT	STRAND 171 178
FT	TURN 179 182
FT	STRAND 183 190
FT	TURN 191 192
FT	STRAND 193 200
FT	TURN 203 205
FT	HELIX 213 215
FT	STRAND 216 221
FT	STRAND 226 230
FT	TURN 234 235
FT	STRAND 237 240
FT	TURN 244 245
FT	STRAND 246 247
FT	STRAND 249 251
FT	STRAND 259 259
FT	STRAND 262 265
FT	CONFLICT 6 6
SQ	SEQUENCE 269 AA; 30747 MW; C8589946 CRC32; K -> E (IN REF. 2).
Query Match 15.4%; Score 200; DB 5; Length 269;	
Best Local Similarity 33.7%; Pred. No. 6.42e-22;	
Matches 31; Conservative 17; Mismatches 42; Indels 2; Gaps	
Ddb	176 lqlkehnlyscvlkddxptlqlesvdpknyp-kkkmekrfvnkfelnkklfesagfp 234    : :           : :     : :     : :     :    : :           : :     : :     : :     :
Oy	86 LGIHGKMCLSCVKGDETRLQLEAVNITDLSENKKQDKRFARISDSGGPTTSFESAACP 145    : :           : :     : :     : :     :
Ddb	235 nvyistsqaempvf1g9-tkgggdittftmq 265    : :           : :     : :     : :     :
Oy	146 GWFLCTAEADQPVSLTNNMPDEGVMTKRYFQ 177    : :           : :     : :     : :     :
RESULT	13
ID	ILIB_FELCA STANDARD; PRT: 267 AA.
AC	P41687;
DT	01-NOV-1995 (REL. 32, CREATED)
DT	01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)

01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).  
IL1B.  
OS FELIS SILVESTRIUS CATUS (CAT).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; CARNIVORA.  
[1]  
RN SEQUENCE FROM N.A.  
RP TISSUE=BONE MARROW;  
RC DANIEL S.L., BRENNER C.A., LEGENDRE A.M., SOLOMAN A., ROUSE B.T.;  
RA SUBMITTED (XX-1993) TO EMBL/GENBANK/DBJ DATA BANKS.  
RL -! FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES  
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL  
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.  
CC IL-1 PROTEIN IS INVOLVED IN THE INFLAMMATORY RESPONSE, BEING  
CC IDENTIFIED AS ENDOGENOUS PYROGEN, AND ARE REPORTED TO STIMULATE  
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOCIAL CELLS.  
CC -! SUBUNIT: MONOMER.  
CC -! THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO  
CC ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.  
CC -! THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR  
CC SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS  
CC SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER  
CC SECRETORY PROTEINS.  
CC -! SIMILARITY: BELONGS TO THE IL-1 FAMILY.  
CC EMBL; M92060; G402365; -.  
DR PROSITE; PS00253; INTERLEUKIN.1.  
DR CYTOKINE; MACROPHAGE; MITOGEN; INFLAMMATORY RESPONSE; PYROGEN.  
KF PROPEP 1 115 BY SIMILARITY.  
FT CHAIN 116 267 INTERLEUKIN-1 BETA.  
FT CARBOHYD 37 37 POTENTIAL.  
FT CARBOHYD 58 58 POTENTIAL.  
FT CARBOHYD 217 217 POTENTIAL.  
SQ SEQUENCE 267 AA; 30361 MW; 0ECC9B96 CRC32;

Query Match 15.3%; Score 198; DB 5; Length 267;  
Best Local Similarity 28.7%; Pred. No. 1.72e-21;  
Matches 41; Conservative 34; Mismatches 59; Indels 9; Gaps 6;

Db 121 qdytfdrdisckslvsgsyelralhngnmqgvfmsfwhgeenskkipvciikkn 180  
QY 39 QAFRIWDVWVKQTFYLRNN-OLVAGYLQGGPNVLEE--KIDVVPVPIBPA--L--FLGIHGG 91  
Db 181 nlylscvmkgdkptqlqleml-d-pkyvppkkmekrfvfknteikgnvefessqfnpwivist 239  
QY 92 KWCLSVCVSGDETRQLQLEAVNITDLSSENKQDKRAFIRSDSGPTSFESAACPGWFLCT 151  
240 sqaeeempvflgn-tkxggqdtdf 261  
QY 152 AMEADQPVSLTNPDGVMVTKF 174

RESULT 14  
ID IL1B-RABIT STANDARD; PRT; 268 AA.  
AC P14628;  
DT 01-APR-1990 (REL. 14, CREATED)  
DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)  
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA) (LYMPHOCYTE PROLIFERATION  
DE POTENTIATING FACTOR).  
GN IL1B.  
OS ERYCOTYLUS CUNICULUS (RABBIT).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; LAGOMORPHA.  
[1]  
RN SEQUENCE FROM N.A.  
RP MEDLINE; 89176242.  
RX CANNON J.G., CLARK B.D., WINGFIELD P., SCHWEISSNER U., LOSBERGER C.,  
RA DINARELLO C.A., SHAW A.R.;  
RL J. IMMUNOL. 142:2299-2306(1989).  
[2]  
RN SEQUENCE FROM N.A.  
RP MEDLINE; 88134238.

MORI S., GOTO F., GOTO K., OHKAWARA S., MAEDA S., SHIMADA K.,  
YOSHINAGA M.;  
BIOCHEM. BIOPHYS. RES. COMMUN. 150:1237-1243(1988).  
[3]  
SEQUENCE FROM N.A.  
MEDLINE: 89315718.  
RA YOUNG P.R., SYLVESTER D.;  
RA PROTEIN ENG. 2:545-551(1989).  
CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES  
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL  
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.  
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING  
CC IDENTIFIED AS ENDOGENOUS PYROGEN, AND ARE REPORTED TO STIMULATE  
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.  
CC -!- SUBUNIT: MONOMER.  
CC -!- THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO  
CC ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.  
CC -!- THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR  
CC SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS  
CC SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER  
CC SECRETORY PROTEINS.  
CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.  
CC EMBL: D21835; G452204; -;  
DR EMBL: M26295; G516633; -;  
DR PIR: A27714; A27714.  
DR PIR: J00082; J00082.  
DR PIR: A30584; A30584.  
DR HSP: P01584; IHTB.  
DR PROSITE: P500253; INTERLEUKIN-1.  
DR CYTOKINE; MACROPHAGE; MITOGEN; INFLAMMATORY RESPONSE; PYROGEN.  
KW PROPEP 1 116  
FT CHAIN 117 268 INTERLEUKIN-1 BETA.  
FT CARBOHYD 58 58 POTENTIAL.  
FT CARBOHYD 251 251 POTENTIAL.  
SQ SEQUENCE 268 AA; 30665 MW; E9C910FE CRC32;  
  
Query Match 15.0%; Score 195; DB 5; Length 268;  
Best Local Similarity 37.2%; Pred. No. 7.49e-21;  
Matches 29; Conservative 16; Mismatches 33; Indels 1; Gaps  
  
Ddb 175 lglrgknlyscvmdkdpkltqlqesvd-puryppkkmekrfvfnkldkldkfesaqfp 233  
QY ||::: ||||: | ||||: |::: ||||: |::: ||||: |::: ||||: |  
86 LGTHGGKMLCSVKGDETRLEAVNTIDLSNRKQKRFARFIRSDGPTTFSESAACP 145  
  
Ddb 234 nvyistsqteymvpvflgn 251  
QY ||::: ||||: | ||||: |  
146 GWFLCTAMEADQFVSLTN 163  
  
RESULT 15  
ID IL1B\_CERTO STANDARD; PRT; 269 AA.  
AC P46648;  
01-NOV-1995 (REL. 32, CREATED)  
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)  
DE 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).  
GN IL1B.  
OS CERCOBESUS TORQUATUS ATYS (RED-CROWNED MANGABEY) (SOOTY MANGABEY).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
OC [1]  
RC SEQUENCE FROM N.A.  
RX TISSUE-BLOOD;  
RX MEDLINE: 96003435.  
RA VILLINGER F.J., BRAR S.S., MAYNE A.E., CHIKALA N., ANSARI A.A.;  
RA J. IMMUNOL. 155:3946-3954(1995).  
CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES  
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL  
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.  
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING  
CC IDENTIFIED AS ENDOGENOUS PYROGEN, AND ARE REPORTED TO STIMULATE  
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.  
CC -!- SUBUNIT: MONOMER



CC -!- THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO  
 CC ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.  
 CC -!- THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR  
 CC SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS  
 CC SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER  
 CC SECRETORY PROTEINS.  
 CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.  
 DR EMBL; U19837; G644792; -  
 DR PROSITE; PS00253; INTERLEUKIN\_1.  
 KW CYTOKINE; MACROPHAGE; MITOGEN; INFLAMMATORY RESPONSE; PYROGEN.  
 FT PROPEP 1 116 BY SIMILARITY.  
 FT CHAIN 117 269 INTERLEUKIN-1 BETA.  
 SQ SEQUENCE 269 AA; 30445 MW; F1397FAE CRC32;  
 Query Match 14.2%; Score 184; DB 5; Length 269;  
 Best Local Similarity 32.6%; Pred. NO. 1.57e-18;  
 Matches 30; Conservative 18; Mismatches 42; Indels 2; Gaps 2;  
 Db 176 lgikaknlvlsclvldkptlqliesvdpkayp-kkmekrfvfnkknklecesadfp 234  
 86 LGIHGKMKCLSCVKSGDETRQLQLEAVNITDLSENKQDKRFAFIRSDSGPTTSFSAACP 145  
 235 nwyistsqaenmpvflggtgrg-gqditdftmq 265  
 QY 146 GWFLCTAMEADQPVSLTNMPDEGVWTKFYEQ 177

Search completed: Thu Feb 19 10:11:16 1998  
 Job time : 22 secs.

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WATERMAN

(TM)

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MPSrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm  
Run on: Thu Feb 19 09:38:05 1998; MasPar time 625.32 Seconds  
1315.209 Million cell updates/sec  
Output not generated.

Title: >US-08-910-733-12  
Description: (1-579) from US08910733.seq  
Perfect Score: 579  
N.A. Sequence: 1 CAGAGGAGCTCTGTCCTA.....TCCAGGAGGAGGAGTAGTAC 579  
Comp: GTCTTCTCGGAGGACAGGAT.....AGTCTCTGCTGCTCATCATG

Scoring table: TABLE default  
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 430261 seqs, 710217276 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: emb1-new7  
1: BCT 2: FUN 3: GEN 4: HTG1 5: HTG2 6: HTG3 7: HTG4 8: HUM1  
9: HUM2 10: HUM3 11: INV1 12: INV2 13: ORG 14: MAM 15: VRT  
16: PLN 17: PRO1 18: PRO2 19: ROD 20: SYN 21: UNC 22: VIR  
genbankai101  
23: BCT1 24: BCT2 25: BCT3 26: BCT4 27: BCT5 28: BCT6 29: BCT7  
30: BCT8 31: BCT9 32: BCT10 33: BCT11 34: BCT12 35: BCT13  
36: GEN1 37: GEN2 38: GEN3 39: GEN4 40: GEN5 41: GEN6 42: HTG1  
43: HTG2 44: HTG3 45: HTG4 46: HTG5 47: INV1 48: INV2 49: INV3  
50: INV4 51: INV5 52: INV6 53: INV7 54: INV8 55: INV9 56: INV10  
57: INV11 58: INV12 59: MAM1 60: MAM2 61: MAM3 62: VRT1  
63: VRT2 64: VRT3 65: VRT4 66: PAT1 67: PAT2 68: PAT3 69: PAT4  
70: PAT5 71: PAT6 72: PAT7 73: PHG 74: PLN1 75: PLN2 76: PLN3  
77: PLN4 78: PLN5 79: PLN6 80: PLN7 81: PLN8 82: PLN9 83: PLN10  
84: PLN11 85: PLN12 86: PRI1 87: PRI2 88: PRI3 89: PRI4  
90: PRI5 91: PRI6 92: PRI7 93: PRI8 94: PRI9 95: PRI10  
96: PRI11 97: PRI12 98: PRI13 99: PRI14 100: PRI15 101: PRI16  
102: PRI17 103: ROD1 104: ROD2 105: ROD3 106: ROD4 107: ROD5  
108: ROD6 109: ROD7 110: ROD8 111: ROD9 112: STR 113: SYN  
114: UNA  
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115: VRL1 116: VRL2 117: VRL3 118: VRL4 119: VRL5 120: VRL6  
121: VRL7 122: VRL8 123: VRL9 124: VRL10 125: VRL11  
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126: BCT 127: GEN 128: HTG1 129: HTG2 130: INV 131: MAM  
132: VRT 133: PHG 134: PLN1 135: PLN2 136: PRI1 137: PRI2  
Database: u-emb151\_101  
142: part1 143: part2

Database: genbankb101  
115: VRL1 116: VRL2 117: VRL3 118: VRL4 119: VRL5 120: VRL6  
121: VRL7 122: VRL8 123: VRL9 124: VRL10 125: VRL11  
genbank-new7  
126: BCT 127: GEN 128: HTG1 129: HTG2 130: INV 131: MAM  
132: VRT 133: PHG 134: PLN1 135: PLN2 136: PRI1 137: PRI2  
Database: u-emb151\_101  
142: part1 143: part2

Statistics: Mean 10.706; Variance 5.142; scale 2.082

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	579	100.0	579 143	A50279	Sequence 13 from Paten	0.00e+00
2	573	99.0	578 91	HSILIRAI1	H.sapiens mRNA for in	0.00e+00
3	474	81.9	474 143	A50276	Sequence 10 from Paten	0.00e+00
4	474	81.9	540 70	I09592	Sequence 3 from Paten	0.00e+00
5	474	81.9	1684 91	HSILIRAP	H.sapiens mRNA for in	0.00e+00
6	474	81.9	1740 91	HSILIRA	H.sapiens mRNA for in	0.00e+00
7	472	81.5	600 70	I09594	Sequence 8 from Paten	0.00e+00
8	472	81.5	600 70	I08135	Sequence 3 from Paten	0.00e+00
9	471	81.3	602 99	HUMILIRAA	Human icIL-1ra mRNA,	0.00e+00
10	470	81.2	540 70	I09591	Sequence 1 from Paten	0.00e+00
11	469	81.0	534 99	HOMILRA	Human interleukin 1 r	0.00e+00
12	468	80.8	531 142	A50144	Sequence 1 from Paten	0.00e+00
13	468	80.8	531 142	A49726	Sequence 1 from Paten	0.00e+00
14	322	55.6	563 61	PIGIRAP	Sus scrofa (clone p03	7.53e-246
15	319	55.1	1594 61	RABILIRAI	Rabbit mRNA for inter	3.18e-243
16	319	55.1	1612 61	RABILIRAB	Rabbit interleukin 1	3.18e-243
17	317	54.7	574 61	S68977	sIL-1ra-interleukin-1	1.79e-241
18	296	51.1	542 111	S64082	interleukin 1 recepto	4.06e-223
19	296	51.1	1576 108	MUSILIRAA	Mouse interleukin 1 r	4.06e-223
20	296	51.1	1877 108	MUSILIRN	Mouse IL-1rn antagoni	4.06e-223
21	296	51.1	1940 108	MUSILIRA	Mus domesticus interl	4.06e-223
22	293	50.6	520 108	MUSILIRA	Musculus interleuki	1.69e-220
23	269	46.5	537 109	RATILRA	Rat interleukin 1 rec	5.32e-158
24	221	38.2	12565 137	HSILIRECA	H.sapiens gene for in	5.32e-158
25	221	38.2	12565 91	HSILIRECA	H.sapiens gene for in	5.32e-158
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27	186	32.1	270 70	I08134	Sequence 1 from Paten	6.08e-128
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29	131	22.6	6350 108	MUSILIRN	Mouse germline interl	1.92e-81
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31	72	12.4	99 143	A50274	Sequence 8 from Paten	1.34e-33
32	37	6.4	42 143	A50272	Sequence 6 from Paten	4.89e-08
33	37	6.4	2172 91	HSICILIRA	H.sapiens IL-1ra gene	4.89e-08
34	32	5.5	465 67	A32116	Synthetic (126Ala,128	7.82e-05
35	32	5.5	986 68	E01591	CDNA encoding human i	7.82e-05
36	31	5.4	944 59	BOVILIBA	Bovine interleukin 1-	3.24e-04
37	31	5.4	944 59	BTILIBR	Bovine mRNA for inter	3.24e-04
38	31	5.4	1736 59	BOVILIB	Bovine interleukin 1-	3.24e-04
39	31	5.4	1750 69	I03510	Sequence 1 from Paten	3.24e-04
40	30	5.2	465 67	A32000	Synthetic IL-1 beta g	1.31e-03
41	30	5.2	1124 91	HSILIBR	Human mRNA for interl	1.31e-03
42	30	5.2	1469 69	I01156	Sequence 1 from Paten	1.31e-03
43	30	5.2	1507 70	I07942	Sequence 1 from Paten	1.31e-03
44	30	5.2	1507 68	E00846	CDNA sequence for hum	1.31e-03
45	30	5.2	1514 69	I00729	Sequence 2 from Paten	1.31e-03

ALIGNMENTS

RESULT 1  
ID A50279 standard; DNA; UNC; 579 BP.  
AC A50279;  
NI ei039152  
DT 07-MAR-1997 (Rel. 51, Created)  
DE 07-MAR-1997 (Rel. 51, Last updated, Version 1)  
DS Sequence 13 from Patent WO9612022.  
KW .  
OS unidentified  
OC OS  
RN [1]  
RP 1-579  
RA Colotta F., Muzio M., Mantovani A.;  
RT "INTRACELLULAR ISOFORM OF THE INTERLEUKIN-1 RECEPTOR  
RL ANTAGONIST";  
RL Patent number WO9612022-A/13, 25-APR-1996.  
RL APPLIED RESEARCH SYSTEMS (NL).

CC Other publication AU 3841795 960506  
FH Key Location/Qualifiers  
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FT MEDLINE 34..573 /db\_xref="PID:e306485"  
FT CDS /translation="MALADYEGGGGEGEDNADSKETICRPSGRKSKMOAFRIW  
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FT D VNKQTFYLRNNQLVAGYLOGPNVNLKIDVPIEHALFLGIHGGKMLCSVKSGDE  
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FT N RQLEAVNITDLSNRKQDKRFAIRSDSPTTSFESAACPGWFLCTAMEADQPVSLT  
FT SQ MPDEGVNMTKFFQDEE"  
SQ Sequence 579 BP; 157 A; 146 C; 155 G; 121 T; 0 other;

Query Match 100.0%; Score 579; DB 143; Length 579;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 61 ggaaggaggag 120  
QY 61 GGAGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120  
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QY 241 TTGAAGAAAGATAGATGT 300  
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QY 361 GCAGTTTAACATCACTGACCTGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
Db 421 cgtcagacagtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 480  
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Db 481 tgcacagcagatgaagctgacagcagcagcagcagcagcagcagcagcagcagcagcagc 540  
QY 481 TGCAACGCGATGAAGCTGACAGCGCGCTGAGCGCTGAGCGCTGAGCGCTGAGCGCTGAG 540  
Db 541 atgggtcaccaaatctactctccagagagagagagagagagagagagagagagagagag 579  
QY 541 ATGGTCAACCAATCTACTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 579

RESULT 2  
LOCUS HSIL1RA1 578 bp RNA PRI 04-OCT-1995  
DEFINITION H.sapiens mRNA for intracellular IL-1 receptor antagonist type II.  
ACCESSION X84348  
VERSION 1  
KEYWORDS interleukin 1 receptor.  
359AC5 human.  
ORGANISM Homo sapiens  
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 578)  
AUTHORS Muzio,M., Polentarutti,N., Sironi,M., Poli,G., De Gioia,L.,

Introna,M., Mantovani,A. and Colotta,F.  
Cloning and characterization of a new isoform of the interleukin 1  
receptor antagonist  
J. Exp. Med. 182 (2), 623-628 (1995)  
95355865  
2 (bases 1 to 578)  
Introna,M.  
Direct Submission  
Submitted (01-FEB-1995) M. Introna, Istituto di Ricerche  
Farmacologiche, 'Mario Negri', Via Eritrea 62, 20157 Milano, ITALY  
Location/Qualifiers  
1..578  
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/cell\_type="polymorphonuclear cells"  
33..575  
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BASE COUNT 157 a 146 c 154 g 121 t  
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Query Match 99.0%; Score 573; DB 91; Length 578;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 66 ggaaggaggag 125  
QY 67 GGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 126  
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QY 127 GGGAGAAAATCCAGCAAGATGCAAGCCTTCAGAACTCTGGGATGTAAACAGAAGACCTC 186  
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QY 247 GAAAAGATAGATGT 306  
Db 306 aagatgtcctgtcctgtcctgtcctgtcctgtcctgtcctgtcctgtcctgtcctgtcct 365  
QY 307 AAGATGTGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 366  
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QY 367 AACATCACTGACCTGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 426  
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QY 487 GCGATGAAGCTGACAGCGCTGAGCGCTGAGCGCTGAGCGCTGAGCGCTGAGCGCTG 546  
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ID A50276  
AC A50276;

NI e1039151  
DT 07-MAR-1997 (Rel. 51, Created)  
DE 07-MAR-1997 (Rel. 51, Last updated, Version 1)  
DE Sequence 10 from Patent WO9612022.  
KW unclassified  
OS unclassified  
OC unclassified  
RN [1]  
RP 1-474  
RA Colotta F., Muzio M., Mantovani A.;  
RT "INTRACELLULAR ISOFORM OF THE INTERLEUKIN-1 RECEPTOR  
RT ANTAGONIST";  
RL Patent number WO9612022-A/10, 25-APR-1996.  
RL APPLIED RESEARCH SYSTEMS (NL).  
CC Other publication AD 3841795 960506  
FH Key  
FH Location/Qualifiers  
FT source  
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Query Match 81.9%; Score 474; DB 143; Length 474;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 gatgttaacagaagaccctctctatctgaggaaacaaactagttgctgatacttgc 120  
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Db 121 ggaacaaatgtaattagaagaagatagatggttaacattgagcctcattgctctg 180  
QY 226 GGACCAAAATGTCAATTTAGAAAGAAAGATAGATGCTGCTCTCTGCTCAAGTCTGGTATG 285

Db 181 tctctgggaatccatgagggaagatgctgctctctgctgctgctgctgctgctgctg 240  
QY 286 TTCTTGGGAATCCATCGAGGGAAGATGCTGCTCTCTGCTGCTGCTGCTGCTGCTG 345

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QY 466 CCGGTTGTGTTCTCTGACAGCGATGGAAGCTGACAGCCGCTGACCCCTCACCATA 525

Db 421 cctgacgaaggcgtcatggttcacaaattctacttccagagcagcagtagtagtac 474  
QY 526 CCTGACGAAGGCGTCATGTCACCAATTTCTACTTCCAGGAGGACGAGTAGTAC 579

RESULT 4  
LOCUS I09592 540 bp  
DEFINITION Sequence 3 from Patent WO 8911540.  
ACCESSION I09592  
NID 9587700  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unknown.

Unclassified.  
1 (bases 1 to 540)  
Hannon,C.H., Eisenberg,S.P., Thompson,R.C., Arend,W.p., Joslin,F.G.  
and Sommer,A.  
TITLE INTERLEUKIN-1 INHIBITORS  
JOURNAL Patent: WO 8911540-A 3 30-NOV-1989;  
FEATURES Location/Qualifiers  
source 1..540  
BASE COUNT 135 a 149 c 133 g 123 t  
ORIGIN

Query Match 81.9%; Score 474; DB 70; Length 540;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 27 gagacgatctgcgacccctctgaggagaaatccagcaagatgcaagccttcagaatctgg 86  
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Db 87 gatgttaacagaagaccctctctatctgaggaaacaaactagttgctgatacttgc 146  
QY 166 GATGTTAACAGAAAGACCTTCTATCTGAGGAACAACTAGTTGCTGGATCTTGCAA 225

Db 147 ggaacaaatgtaattagaagaagatagatggttaccattgagcctcattgctctg 206  
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QY 286 TTCTTGGGAATCCATCGAGGGAAGATGCTGCTCTCTGCTGCTGCTGCTGCTGCTG 345

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Db 387 ccggtgtgtctctctgacagcagtgaggatgaggatgaggatgaggatgaggatgagg 446  
QY 466 CCGGTTGTGTTCTCTGACAGCGATGGAAGCTGACAGCCGCTGACCCCTCACCATA 525

Db 447 cctacgaagcgtcagtggtcaccacaaattctacttccagagcagcagtagtagtac 500  
QY 526 CCTGACGAAGGCGTCATGGTCCCAAAATTTACTTCCAGGAGGAGGAGTAGTAC 579

RESULT 5  
LOCUS HSILRAP 1684 bp RNA  
DEFINITION H.sapiens mRNA for IRAP.  
ACCESSION X53296  
NID g32578  
KEYWORDS interleukin 1 receptor antagonist.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Euthera; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 1684)  
Carter,D.B., Delbel,M.R., Dunn,C.J., Tomich,C.S.C., Laborde,A.L.,  
Slightom,J.L., Berger,A.E., Bienkowski,M.J., Sun,F.F., McEwan,R.N.,  
Harris,P.K.W., Yem,A.W., Waszak,G.A., Chosay,J.G., Sieu,L.C.,  
Hardee,M.M., Zurcher-Neely,H.A., Reardon,I.M., Heinrichson,R.L.,  
Truesdell,S.E., Shelly,J.A., Eessalu,T.E., Taylor,B.M. and  
Tracey,D.E.  
Purification, cloning, expression and biological characterization  
of an interleukin-1 receptor antagonist protein  
JOURNAL Nature 344 (6267), 633-638 (1990)  
MEDLINE 90220867  
FEATURES Location/Qualifiers  
source 1..1684  
/organism="Homo sapiens"

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BASE COUNT 396 a 473 c 371 g 444 t
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Best Local Similarity 100.0%; Pred. No. 0.00e+00;
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Qy 466 CCCGGTTGGTTCTCTGCACAGCATGGAAGTGAACGAGCCGCTCAGCCTCACCACATATG 525
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Qy 526 CCTGACGAAGGCGTCATGGTCACCAAAATCTACTTCCAGGAGGAGGAGGAGGAGGAGTAC 579

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RESULT 6
LOCUS HSIIRA 1740 bp RNA PRI 15-OCT-1992
DEFINITION H.sapiens mRNA for interleukin-1 receptor antagonist.
ACCESSION X52015
NID g32576
KEYWORDS interleukin 1 receptor antagonist.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1740)
AUTHORS Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.
Eisenberg, S.P., Evans, R.J., Arend, W.P., Verderber, E., Brewer, M.T.,
Hannum, C.H. and Thompson, R.C.
TITLE Primary structure and functional expression from complementary DNA
of a human interleukin-1 receptor antagonist
MEDLINE Nature 343 (6256), 341-346 (1990)
FEATURES
source Location/Qualifiers
1..1740
/organism="Homo sapiens"

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BASE COUNT 422 a 483 c 384 g 451 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.00e+00;
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Db 147 gatgttaaccagaagacccctctatctgaggagaacaaacaaactagttgctggatacttgc 206
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Qy 406 CGCTTGCCTTCATCCCTCAGACAGTGGCCCAACACACACACACACACACACACACAC 465
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Qy 466 CCCGGTTGGTTCTCTGCACAGCATGGAAGTGAACGAGCCGCTCAGCCTCACCACATATG 525
Db 507 cctgacgaagggctcagtggtacacaaattctacttccagggagggagcagtagtac 560
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RESULT 7
LOCUS IO9594 600 bp PAT 14-NOV-1994
DEFINITION Sequence 8 from Patent WO 8911540.
ACCESSION IO9594
NID g587702
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 600)
AUTHORS Hannum, C.H., Eisenberg, S.P., Thompson, R.C., Arend, W.P., Joslin, F.G.
TITLE INTERLEUKIN-1 INHIBITORS
JOURNAL Patent: WO 8911540-A 8 30-NOV-1989;
FEATURES Location/Qualifiers
source 1..600
/organism="unknown"
BASE COUNT 152 a 167 c 147 g 134 t
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Best Local Similarity 99.8%; Pred. No. 0.00e+00; Matches 473; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
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Db	147	gatgttaacagaagacccttctatctgaggaacaaacaaatagttgctgatacttcaa 206
QY	166	GATGTTAACCAAGAACCTTCTATCTGAGGAACAACCAACTAGTTGCTGGATCTGCAA 225
Db	207	gacacaaatgcaatttagaagaaagatagatgtgtaccattgagcctcatgctctg 266
QY	226	GGACCAAAATGTCAAATTAGAAAGAAAGATAGTGTGTACCCATTGAGCCTCATGCTG 285
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QY	286	TCTTGGGAATCCATGAGGGAAGATGTGCTGTCTGTGTCAGTCTGGTATGAGACC 345
Db	327	agactcagctggagcagcttaacatcaactgagcgcagagacagaaagcaggacaag 386
QY	346	AGACTCAGCTGGAGCAGTTAAACATCACTACCTGAGCGAGAAAGACAGGACAAG 405
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QY	526	CCTGACGAAGCGTCATGGTCAACCAATCTACTTCCAGGAGGAGGAGTAGTAC 579
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LOCUS	HUMILIRAA	602 bp mRNA PRI 06-JAN-1995
DEFINITION	Human icIL-1ra mRNA, complete cds.	
ACCESSION	M55646	
NID	g186291	
KEYWORDS	interleukin 1 receptor antagonist.	
SOURCE	Human epithelial/leukocyte, cDNA to mRNA.	
ORGANISM	Homo sapiens	
REFERENCE	1 (bases 1 to 602)	
AUTHORS	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.	
TITLE	Haskill, S., Martin, G., Van Le, L., Morris, J., Peace, A., Bigler, C.F., Hammerberg, C., Fong, S., Arend, W.P., Ralph, P. and Sporn, S.A. cDNA cloning of an intracellular form of the human Interleukin 1 receptor antagonist associated with epithelium	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 88 (9), 3681-3685 (1991)	
MEDLINE	91219436	
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BASE COUNT	151 a 162 c 159 g 130 t	
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Db	192	gatgttaacagaagacccttctatctgaggaacaaacaaatagttgctgatacttcaa 251
QY	166	GATGTTAACCAAGAACCTTCTATCTGAGGAACAACCAACTAGTTGCTGGATCTGCAA 225
Db	252	ggacacaaatgcaatttagaagaaagatagatgtgtaccattgagcctcatgctctg 311
QY	226	GGACCAAAATGTCAAATTAGAAAGAAAGATAGTGTGTACCCATTGAGCCTCATGCTG 285
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QY	286	TCTTGGGAATCCATGAGGGAAGATGTGCTGTCTGTGTCAGTCTGGTATGAGACC 345
RESULT 8		
LOCUS	I08135	600 bp PAT 14-NOV-1994
DEFINITION	Sequence 3 from Patent EP 0343684.	
ACCESSION	I08135	
NID	g589153	
KEYWORDS	Unknown.	
SOURCE	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 (bases 1 to 600)	
AUTHORS	Hannum, C.H., Eisenberg, S.P., Thompson, R.C., Arend, W.P., Joslin, F.G. and Sommer, A.	
TITLE	Interleukin-1 inhibitors	
JOURNAL	Patent: EP 0343684-A1 3 29-NOV-1989;	
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NID g587699  
KEYWORDS  
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ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 540)  
AUTHORS Hannon,C.H., Eisenberg,S.P., Thompson,R.C., Arend,W.P., Joslin,F.G.  
and Sommer,A.  
TITLE INTERLEUKIN-1 INHIBITORS  
JOURNAL Patent: WO 8911540-A 1 30-NOV-1989;  
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SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 534)  
AUTHORS Eisenberg,S.P., Brewer,M.T., Verderber,E., Heimdal,P.,  
Brandhuber,B.J. and Thompson,R.C.  
TITLE Interleukin 1 receptor antagonist is a member of the interleukin 1  
gene family: evolution of a cytokine control mechanism  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 88 (12), 5232-5236 (1991)  
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DE	07-MAR-1997 (Rel. 51, Last updated, Version 1)		
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OC	Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
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RP	1-531		
RA	Tagliabue A., Boraschi D., Bossu P., Macchia G., Maurizi G.,		
RA	Porzio S., Ruggiero P.,		
RT	"MICROORGANISMS AS THERAPEUTIC DELIVERY SYSTEMS";		
RL	Patent number WO9611277-A/1, 18-APR-1996.		
RL	DOMPE SPA (IT).		
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10-MAR-1997 (Rel. 51, Created)

DT 10-MAR-1997 (Rel. 51, Last updated, Version 1)

DE Sequence 1 from Patent WO9609323.

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OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

OC Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

RN [1]

RP 1-531

RA Boraschi D., Bossu P., Ruggiero P., Macchia G., Tagliabue A.,

RA Frigerio F., Grifantini R., Frascotti G., Grandi G.,

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